

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 09:45:33 ; Search time 2226.25 Seconds
(without alignments)
8496.727 Million cell updates/sec

Title: US-09-996-630A-11_COPY_1_400

Perfect score: 400
Sequence: 1 gctctaaagctgtaagacc.....ccaaatgatgaccaccag 400

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ha: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400	100.0	4165	6	AX329586 Sequence
2	398.4	99.6	2193	6	CQ722611 Sequence
3	398.4	99.6	2298	6	AX166529 Sequence
4	398.4	99.6	4772	6	AX642970 Sequence
5	398.4	99.6	4882	9	HUMKRAAO
6	398.4	99.6	5519	9	AF226044
7	396.8	99.2	5140	9	BC071567
8	323.8	81.0	4708	10	AF387809
9	322.2	80.5	3004	10	RNSNPIKIN
10	322.2	80.5	3101	10	BC020189
11	275	68.8	248901	2	AC118087
12	212	53.0	143034	2	AC104184
13	212	53.0	186485	2	AC138808
14	208.2	52.0	160170	2	AC143769
15	171.8	43.0	194261	10	AC121264
16	171.8	43.0	206641	10	AC120394
17	168.2	42.0	252055	2	AC106612
18	137.2	34.3	1253	5	BC075868
19	130.8	32.7	2834	5	BC060922

20	107.4	26.9	182002	2	AC142030
21	104.4	26.1	149790	9	AC022106
22	104.4	26.1	157076	9	AC010441
23	104.4	26.1	229053	2	AC010309
24	100.2	25.1	546	9	BC038539
25	80.6	20.1	136547	2	AC134966
26	76.6	19.1	199086	2	CR388073
27	72.6	18.1	2860	6	CQ590679
28	72.6	18.1	2969	3	AY095014
29	72.6	18.1	3172	3	AY052073
30	65.4	16.4	534	6	BD168101
31	54.2	13.6	149790	9	AC022106
32	54.2	13.6	157076	9	AC010441
33	54.2	13.6	229053	2	AC010309
34	50	12.5	51	6	CQ001589
35	46.4	11.6	128326	8	AP003756
36	46.4	11.6	157974	8	AP003755
37	43.2	10.8	131711	2	AP003954
38	43.2	10.8	144337	8	AP005320
39	43.2	10.8	152883	8	AP004269
40	43.2	10.8	152883	8	AP004319
41	43	10.8	158574	8	AP003763
42	42	10.5	146458	2	AC134346
43	42	10.5	157009	8	AC137748
44	41.8	10.4	4235	10	BC049083
45	41.8	10.4	104128	10	AL929562

ALIGNMENTS

RESULT 1	AX329586	Sequence 95 from Patent WO0194629.	DNA	Linear	PAT 09-JAN-2002
LOCUS	AX329586	4165 bp			
DEFINITION	Sequence 95 from Patent WO0194629.				
ACCESSION	AX329586				
VERSION	AX329586.1	GI:18102564			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.				
TITLE	Cancer gene determination and therapeutic screening using signature gene sets				
JOURNAL	Patent: WO 0194629-A 95 13-DEC-2001;				
FEATURES	Avallon Pharmaceuticals (US)				
source	1. 4165 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
ORIGIN					
Query Match	100.0%; Score 400; DB 6; Length 4165;				
Best Local Similarity	100.0%; Pred. No. 2.7e-108;				
Matches	400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	GCTTAAAGAGTGTAAAGAGCTTAATTTACACGAGATCTTACAGAGATCTTCCCAAGAGAGGC	60		
Db	1	GCTTAAAGAGTGTAAAGAGCTTAATTTACACGAGATCTTACAGAGATCTTCCCAAGAGAGGC	60		
Qy	61	TTCTTTGAAGAGATTTAAATCATCTTGGCTTACAGAGAGTGGACCTTACACAGTAC	120		
Db	61	TTCTTTGAAGAGATTTAAATCATCTTGGCTTACAGAGAGTGGACCTTACACAGTAC	120		
Qy	121	AAAGTATTAACATTTCCCTTGTGTATTCATCAAAAATTTCTTGGAGAGAGACATCAAGCAT	180		
Db	121	AAAGTATTAACATTTCCCTTGTGTATTCATCAAAAATTTCTTGGAGAGAGACATCAAGCAT	180		
Qy	181	CATTTCAGCGATGTGCTTGGGACATAGCGATTCAGAGCCATTTAGAACCCCTGGA	240		

Db 181 CATTGAGCGATGCTGCTGGGACATGAGCGATGCGAGCGCATTTGTATGAACCCCTGGA 240
Qy 241 AACCAACAGGTATTAACCATATTCACAGCCACATATCTTCTGCTGGCTGAAGAATCCTGAG 300
Db 241 AACCAACAGGTATTAACCATATTCACAGCCACATATCTTCTGCTGGCTGAAGAATCCTGAG 300
Qy 301 AGAAAAGCAAGAGAAAATAACAGACCCAGATCTGCAAGCCGAGCAATATCAAGGCCCA 360
Db 301 AGAAAAGCAAGAGAAAATAACAGACCCAGATCTGCAAGCCGAGCAATATCAAGGCCCA 360
Qy 361 GTTTAGGCACTCATGGCCAAACAAATGATGTACCCCG 400
Db 361 GTTTAGGCACTCATGGCCAAACAAATGATGTACCCCG 400

RESULT 2
LOCUS CQ722611 2193 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 8545 from Patent WO02068579.
ACCESSION CQ722611
VERSION CQ722611.1 GI:42283468
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W., and Myers,B.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
theresof
Patent: WO 02068579-A 8545 06-SEP-2002;
JOURNAL PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1..2193
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 99.6%; Score 398.4; DB 6; Length 2193;
Best Local Similarity 99.8%; Pred. No. 7.9e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCTAAGAGTGTAAAGACCTAATTAACAGGATGCTACAGAGAGATCCCAAGAAAGGCG 60
Db 609 GTCTAAGAGTGTAAAGACCTAATTAACAGGATGCTACAGAGAGATCCCAAGAAAGGCG 668
Qy 61 TTCTTTAGAAGAGATTGAATAATCATCTTGGCTTCAAGGAGTGGAACCTTACACAGCTAC 120
Db 669 TTCTTTAGAAGAGATTGAATAATCATCTTGGCTTCAAGGAGTGGAACCTTACACAGCTAC 728
Qy 121 AAAGTATTAACATTTCCCTTGTGTCTATACAAAATCTCTCGAAGAGAGACCAACAGCAT 180
Db 729 AAAGTATTAACATTTCCCTTGTGTCTATACAAAATCTCTCGAAGAGAGACCAACAGCAT 788
Qy 181 CATTGAGCGATGCTGCTGGGACATGAGCGATTCAGAGCCGATTTGTAGAACCCTGGA 240
Db 789 CATTGAGCGATGCTGCTGGGACATGAGCGATTCAGAGCCGATTTGTAGAACCCTGGA 848
Qy 241 AACCAACAGGTATTAACCATATTCACAGCCACATATCTTCTGCTGGCTGAAGAATCCTGAG 300
Db 849 AACCAACAGGTATTAACCATATTCACAGCCACATATCTTCTGCTGGCTGAAGAATCCTGAG 908
Qy 301 AGAAAAGCAAGAGAAAATAACAGACCCAGATCTGCAAGCCGAGCAATATCAAGGCCCA 360
Db 909 AGAAAAGCAAGAGAAAATAACAGACCCAGATCTGCAAGCCGAGCAATATCAAGGCCCA 968
Qy 361 GTTTAGGCACTCATGGCCAAACAAATGATGTACCCCG 400
Db 969 GTTTAGGCACTCATGGCCAAACAAATGATGTACCCCG 1008

RESULT 3
LOCUS AX166529 2298 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 20 from Patent WO0138503.
ACCESSION AX166529
VERSION AX166529.1 GI:14546874
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Plowman,G.D., Myhre,D., Manning,G.S., Sudareanann,S.S., Martinez,R.,
Planagen,P. and Clary,D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 20 31-MAY-2001;
Sugen, Inc. (US)
FEATURES
source Location/Qualifiers
1..2298
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 99.6%; Score 398.4; DB 6; Length 2298;
Best Local Similarity 99.8%; Pred. No. 7.9e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCTAAGAGTGTAAAGACCTAATTAACAGGATGCTACAGAGAGATCCCAAGAAAGGCG 60
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Qy 61 TTCTTTAGAAGAGATTGAATAATCATCTTGGCTTCAAGGAGTGGAACCTTACACAGCTAC 120
Db 774 TTCTTTAGAAGAGATTGAATAATCATCTTGGCTTCAAGGAGTGGAACCTTACACAGCTAC 833
Qy 121 AAAGTATTAACATTTCCCTTGTGTCTATACAAAATCTCTCGAAGAGAGACCAACAGCAT 180
Db 834 AAAGTATTAACATTTCCCTTGTGTCTATACAAAATCTCTCGAAGAGAGACCAACAGCAT 893
Qy 181 CATTGAGCGATGCTGCTGGGACATGAGCGATTCAGAGCCGATTTGTAGAACCCTGGA 240
Db 894 CATTGAGCGATGCTGCTGGGACATGAGCGATTCAGAGCCGATTTGTAGAACCCTGGA 953
Qy 241 AACCAACAGGTATTAACCATATTCACAGCCACATATCTTCTGCTGGCTGAAGAATCCTGAG 300
Db 954 AACCAACAGGTATTAACCATATTCACAGCCACATATCTTCTGCTGGCTGAAGAATCCTGAG 1013
Qy 301 AGAAAAGCAAGAGAAAATAACAGACCCAGATCTGCAAGCCGAGCAATATCAAGGCCCA 360
Db 1014 AGAAAAGCAAGAGAAAATAACAGACCCAGATCTGCAAGCCGAGCAATATCAAGGCCCA 1073
Qy 361 GTTTAGGCACTCATGGCCAAACAAATGATGTACCCCG 400
Db 1074 GTTTAGGCACTCATGGCCAAACAAATGATGTACCCCG 1113

RESULT 4
LOCUS AX642970 4772 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 47 from Patent WO01096547.
ACCESSION AX642970
VERSION AX642970.1 GI:28550119
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
Gandhi,A.R., Tribouley,C.M., Wallis,N., Yao,M.G., Lu,D.A.,
Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,

Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,
Hafalla,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,
Reichgen,S.A., Azimzai,Y., Policky,J.B., Ding,L., Greiner,M.,
Elliot,C.V.S., Thangaveilu,K., Batra,S. and Ison,C.H.
Human Kinases
Patent: WO 01096547-A 47 20-DEC-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers

FEATURES

Source

1..4772
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 063497CB1"

ORIGIN

Query Match 99.6%; Score 398.4; DB 6; Length 4772;
Best Local Similarity 99.8%; Pred. No. 8e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTAAAGAGTGTAAAGACCTTAATTAACCGGATGCTACAGAGATCCCAAGAGAGGCG 60
DB 910 GTCCTAAAGAGTGTAAAGACCTTAATTAACCGGATGCTACAGAGATCCCAAGAGAGGCG 969
QY 61 TTCTTGAAGAGATTGAAATCATCTTGGCTCAGGAGTGGACCTTCACCAAGCTAC 120
DB 970 TTCTTGAAGAGATTGAAATCATCTTGGCTCAGGAGTGGACCTTCACCAAGCTAC 1029
QY 121 AAAGTATTAACATCTCCCTTGTGTCAATCAAAATCTCTCGAAGAGAGCAACAGCAT 180
DB 1030 AAAGTATTAACATCTCCCTTGTGTCAATCAAAATCTCTCGAAGAGAGCAACAGCAT 1089
QY 181 CATTCAGGAGTGTGTCTGGGAGCATAGCGGATCGAGACCCCATTTGAGAGGCTTCGA 240
DB 1090 CATTCAGGAGTGTGTCTGGGAGCATAGCGGATCGAGACCCCATTTGAGAGGCTTCGA 1149
QY 241 AACCAAGAGTATTAACCATATCAAGCAGCATCTTCTGTGGCTGAAAGATCTTGAG 300
DB 1150 AACCAAGAGTATTAACCATATCAAGCAGCATCTTCTGTGGCTGAAAGATCTTGAG 1209
QY 301 AGAAAGCAGAGAGAAAGAAATACAGACCATCTGCAAGCCCGAACAATATCAAGGCCCA 360
DB 1210 AGAAAGCAGAGAGAAAGAAATACAGACCATCTGCAAGCCCGAACAATATCAAGGCCCA 1269
QY 361 GTTTAGGAGTCAATGCGCAACCAAAATTTGATGTACCCAG 400
DB 1270 GTTTAGGAGTCAATGCGCAACCAAAATTTGATGTACCCAG 1309

RESULT 5

HMK11A0

LOCUS HMK11A0 4882 bp mRNA linear PRI 10-MAY-2002
DEFINITION Human mRNA for KIAA0096 gene, partial cds.
ACCESSION D43636
VERSION D43636.2 GI:20521877
KEYWORDS KIAA0096
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1. Nagase,T., Miyajima,N., Tanaka,A., Sazuka,T., Seki,N., Sato,S.,
Tabata,S., Ishikawa,K.-I., Kawababayashi,Y., Kotani,H. and Nomura,N.
Prediction of the coding sequences of unidentified human genes.
11. The coding sequences of 40 new genes (KIAA0081-KIAA0120)
deduced by analysis of cDNA clones from human cell line KG-1

TITLE

JOURNAL MEDLINE
PUBMED 95108125
7788527
2 (bases 1 to 4882)
Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
Direct Submission
Submitted (24-NOV-1994) Otsu Ohara, Kazuo DNA Research Institute;
1532-3, Yana, Kitarazu, Chiba 292-0812, Japan

(E-mail:cdnainfo@kazuo.or.jp, Tel:+81-438-52-3913)
On May 9, 2002 this sequence version replaced gi:596957.
Location/Qualifiers

FEATURES

Source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ha01240a1"
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/cell_type="myeloblast"
/tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
/note="This sequence was obtained by subcloning of the DNA
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derived from a RT-PCR product (lung) and 1014 - 4882 was
derived from ha01240)."
1..4882
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/note="KIAA0096 gene product is related to a protein
kinase."
/protein_id="BA007744.2"
/db_xref="GI:20521878"
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DYIMKEHGLNEDLAKKYPFAQIVHAISYCHKLAVKDLPEHVVPEFKGLV,LPF
GSNKPFGPKLTLTSCSLAYSAPEILIGEVYAPADIVSLGVLLEMLVCGOPFDB
ANDSETLTMIDCKYTPSHVSKKCDLITRM,ORDPKRRA,SLERIEHNPMLGCVDS
PARKYINPLVSYKQLSEBHNSTIQRVNVLGDIDRDAIVALTNRNHTATYFLLA
ERILREKQKEITGRSAPSNITAGRFQSPFTKIDVQDLEDDLTATPLSHATVPOS
ARADSVLNRKSGK,CDKAKKDLPELAGPLATVPPALPKPAGSGKCLFVEBDE
EBDEBDEKPMSTLOVTLRRKPSVTNRLTSRKSAPLYNQIFEEGSDDEEDMENLPP
KLRLKNKINISPGTVHRRYHRRKSGGSSSESTSDDSRRRLDQSGPFTSWH
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CDS

gene

ORIGIN

Query Match 99.6%; Score 398.4; DB 9; Length 4882;
Best Local Similarity 99.8%; Pred. No. 8e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTAAAGAGTGTAAAGACCTTAATTAACCGGATGCTACAGAGATCCCAAGAGAGGCG 60
DB 718 GCTTAAAGAGTGTAAAGACCTTAATTAACCGGATGCTACAGAGATCCCAAGAGAGGCG 777
QY 61 TTCTTGAAGAGATTGAAATCATCTTGGCTCAGGAGTGGACCTTCACCAAGCTAC 120
DB 778 TTCTTGAAGAGATTGAAATCATCTTGGCTCAGGAGTGGACCTTCACCAAGCTAC 837
QY 121 AAAGTATTAACATCTCCCTTGTGTCAATCAAAATCTCTCGAAGAGAGCAACAGCAT 180
DB 838 AAAGTATTAACATCTCCCTTGTGTCAATCAAAATCTCTCGAAGAGAGCAACAGCAT 897
QY 181 CATTCAGGAGTGTGTCTGGGAGCATAGCGGATCGAGACCCCATTTGAGAGGCTTCGA 240
DB 898 CATTCAGGAGTGTGTCTGGGAGCATAGCGGATCGAGACCCCATTTGAGAGGCTTCGA 957
QY 241 AACCAAGAGTATTAACCATATCAAGCAGCATCTTCTGTGGCTGAAAGATCTTGAG 300
DB 958 AACCAAGAGTATTAACCATATCAAGCAGCATCTTCTGTGGCTGAAAGATCTTGAG 1017
QY 301 AGAAAGCAGAGAGAAAGAAATACAGACCATCTGCAAGCCCGAACAATATCAAGGCCCA 360
DB 1018 AGAAAGCAGAGAGAAAGAAATACAGACCATCTGCAAGCCCGAACAATATCAAGGCCCA 1077
QY 361 GTTTAGGAGTCAATGCGCAACCAAAATTTGATGTACCCAG 400
DB 1078 GTTTAGGAGTCAATGCGCAACCAAAATTTGATGTACCCAG 1117

RESULT 6
AF226044
LOCUS AF226044 5519 bp mRNA linear PRI 20-JUL-2000
DEFINITION Homo sapiens HSNFRK (HSNFRK) mRNA, complete cds.
ACCESSION AF226044
VERSION AF226044.1 GI:9295326
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 5519)
Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z., and Han, Z.
A novel gene expressed in human adrenal gland
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 5519)
Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z., and Han, Z.
TITLE Direct Submission
AUTHORS Submitted (19-JAN-2000) Chinese National Human Genome Center at
TITL Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
JOURNAL Shanghai 201203, P. R. China
LOCATION/Qualifiers
1. 5519
/organism="Homo sapiens"
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/feature_type="adrenal gland"
1. 5519
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ROSSBPPSGSEGGQGSQSPNASGVDNAPSBNNAAGSGSPSGNPTSGTTR
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SVNIGRNPREGLICASSPASCCHTV"

ORIGIN

Query Match 99.6%; Score 398.4; DB 9; Length 5519;
Best Local Similarity 99.8%; Pred. No. 8e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTTAAGAGTGTAAAGACTTAATTACAGGAGTCTACAGAGAGATCCCAAGAAAGGC 60
DB 1355 GCTTAAGAGTGTAAAGACTTAATCAACAGAGTCTACAGAGAGATCCCAAGAAAGGC 1414
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DB 1415 TTCTTAGAAGAGATGAAATCATGCTTGGCTTCAAGGAGTGAACCTTCAACACTTAC 1474
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DB 1475 AAAGTAAACATTCCTCTGTGTGCATACAAAAATCTCTCGAAGAGAGACAAACAGCAT 1534
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DB 1535 CATTCAGCGCATGTGCTTGGGACATAGCGGATCGAAGAGCCATTGTAGAACCTTGA 1594

QY 241 AACCAACAGATTAACCATATATACAGCCACATACCTTCTGTGGCTGAAGATCCTGAG 300
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QY 301 AGAAAAGCAAGAGAAAAGAAATACAGACAGATCTGCAACCCCGAGCAATATCAAGGCCCA 360
DB 1655 AGAAAAGCAAGAGAAAAGAAATACAGACAGATCTGCAACCCCGAGCAATATCAAGGCCCA 1714
QY 361 GTTTAGGAGTCAATGGCCCAACCAAAATTAATGATACCCCGAG 400
DB 1715 GTTTAGGAGTCAATGGCCCAACCAAAATTAATGATACCCCGAG 1754

RESULT 7
BC071567 5140 bp mRNA linear PRI 25-JUN-2004
LOCUS BC071567
DEFINITION Homo sapiens SNF-1 related kinase, mRNA (CDNA clone MGC:87067
IMAGE:4375623), complete cds.
ACCESSION BC071567
VERSION BC071567.1 GI:47939483
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 5140)
Struhsberg, R.L., Feingold, R.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buecaw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Dietchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Kana, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Scherer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 5140)
12477932
Struhsberg, R.
Direct Submission
Submitted (01-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK

COMMENT
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shikari
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@pax11.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAX Plate: 167 Row: b Column: 13
This clone was selected for full length sequencing because it

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RIILREKOEKEIQRSSASPSNIIKAPROSMPKIDVDODLEDLTLATPLSHATVQSPA
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EDEDKPKMSLTQVTLRRKPSVTNRLTSRKSAVUNOIFEEBSDEPMDNLPRK
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CAGPSSNMOIASAGELVLSLKLMLCLGSDLHGASTKYIIDPNGLSPSSVVOEK
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ORIGIN

Query Match 99.2%; Score 396.8; DB 9; Length 5140;
Best Local Similarity 99.5%; Pred. No. 2.4e-107;
Matches 398; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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958 GCTTAAAGAGTGTAAAGCCTAATTAACGCGATGCTTACAGAGATCCCAAGAGAAGGCG 1017
61 TTCTTTAGAGAGATTGAATCATCTTGCTTCAAGGAGTGAACCTTACAGAGCTAC 120
1018 TTATTTAGAGAGATTGAATCATCTTGCTTCAAGGAGTGAACCTTACAGAGCTAC 1077
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1078 AAAGTATPAACATTCCTTGTGTATCAAAAATCTCTCGGAAGAGAGACAACAGCAT 1137
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1138 CATTACAGGATGCTGCTGGGGAATAGAGCGGATCGAGACCTTGAAGAGCGCTGGA 1197
241 AACCAAGAGTATTAACATATCAGAGCACTAATCTTCTGCTGCTGCTGCTGCTGAG 300
1198 AACCAAGAGTATTAACATATCAGAGCACTAATCTTCTGCTGCTGCTGCTGCTGAG 1257
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1258 AGAAAGCAAGAGAAAGAAATACAGACCAATCTGCAAGCCGAGCAATATCAAGGCCCA 1317
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1318 GTTAAAGCAGTCAAGCCCAACCAAAATGATGATACCCAG 1357

RESULT 8
AF387809

LOCUS AF387809 4708 bp mRNA linear ROD 13-SEP-2002
DEFINITION Mus musculus strain BALB/c SNF-1 related kinase (Snrk) mRNA.

ACCESSION

AF387809

VERSION

complete cds.

KEYWORDS

AF387809.2 GI:16418486

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 4708)

AUTHORS

Kertesz, N., Samson, J., Debacher, C., Wu, H. and Labastie, M.-C.

TITLE

Cloning and characterization of human and mouse SNRK sucrose

JOURNAL

non-fermenting protein (SNF-1)-related kinases

REFERENCE

Gene 294 (1-2), 13-24 (2002)

AUTHORS

Labastie, M.-C. and Samson, J.

JOURNAL

Submitted (01-JUN-2001) Institut d'Embryologie Cellulaire et

REFERENCE

Molecular, CNRS et College de France, 49 bis, Ave. de la Belle

AUTHORS

Gabrielle, Ngent Sur Marine 94130, France

JOURNAL

Submitted (25-OCT-2001) Institut d'Embryologie Cellulaire et

REFERENCE

Molecular, CNRS et College de France, 49 bis, Ave. de la Belle

AUTHORS

Labastie, M.-C. and Samson, J.

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Submitted (25-OCT-2001) Institut d'Embryologie Cellulaire et

REFERENCE

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AUTHORS

Labastie, M.-C. and Samson, J.

JOURNAL

Submitted (25-OCT-2001) Institut d'Embryologie Cellulaire et

Db 922 CTCCTGGAAGAGATGAAAGCACCCTTGCTCCAGGAGTGGACCCATCACAGCCAC 981
QY 121 AAGATTAACATCCCTCTGTCATACAAAATCTCTGGAAGAGACCAACAGCAT 180
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RESULT 9
RNSNFKIN 3004 bp mRNA linear ROD 29-FEB-1996
LOCUS R.norvegicus mRNA for SNF1-related kinase.
DEFINITION X89383
VERSION X89383.1 GI:1213223
KEYWORDS SNF1-related kinase; snrk gene.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1
REFERENCE
AUTHORS Becker, W., Heukelbach, J., Kentrup, H. and Joest, H.G.
TITLE Molecular cloning and characterization of a novel mammalian protein
kinase harboring a homology domain that defines a subfamily of
serine/threonine kinases
JOURNAL Eur. J. Biochem. 235 (3), 736-743 (1996)
MEDLINE 8654423
PUBMED 9618453
REFERENCE 2 (bases 1 to 3004)
AUTHORS Heukelbach, J.
TITLE Direct Submision
SUBMITTED (03-JUL-1995) J. Heukelbach, Institut fuer Pharmakologie
und Toxik., der RWTH Aachen, Wendlingweg 2, D-52057 Aachen, FRG
JOURNAL Location/Qualifiers
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ORIGIN

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Matches 351; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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RDSSEGPDSBEGGOSKPSGGGVVDNAPSGDSGTGGGGGGGTGAGTSSSRRC
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SCCHYI"

QY 1 GTCTAAAGAGTGTAAAGACCTTAATTAACAGGATGCTACAGAGATGCCAAGAAAGGC 60
Db 863 GTCTGACGGGTGACAGGACCTCATCACAGGATGCTGACAGAGACCCCAAGAGAGAC 922
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Db 1163 AGAAAGCAAGAGAAAGAAATACAGACCGATTCGACAGCCCAAGATATCAAGCCCA 1222
QY 361 GTTTAGGACATCATGGCCCAACCAAAATGTATGATACCCCA 399
Db 1223 GTTTAGGACATCATGGCCCAACCAAAATGTATGATACCCCA 1261

RESULT 10
LOCUS BC020189 3101 bp mRNA linear ROD 29-JUN-2004
DEFINITION Mus musculus SNF related kinase, mRNA (cDNA clone MGC:28970
IMAGE:4482701), complete cds.
ACCESSION BC020189
VERSION BC020189.1 GI:18043575
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3101)
REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, C.M., Schuler, G.D.,
Altshuler, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uedl, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Kuzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, U., Helton, E., Kettelman, W., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
JOURNAL
TITLE
JOURNAL

REMARK
COMMENT

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 3101)
Strauberg, R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Talia Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prahbu, Parvaneh Saeedi, Jr Santos, Angelique Scherch, Ursula Skalska, Diane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAX Plate: 38 Row: b Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19526941.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="MGC:28970 IMAGE:4482701"
/tissue_type="mammary tumor, Metastatic melanoma-TGF alpha model, 10 month old virgin mouse. Taken by biopsy."
/clone_id="NCI CGAP_Mam1"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6"
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/gene="Snrk"
/note="synonyms: E030034B15, MGC28970, mKIA0096"
/db_xref="locusid:20623"
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FEATURES

SOURCE

CDS

gene

ORIGIN
Query Match 80.5%; Score 322.2; DB 10; Length 3101;
Best Local Similarity 88.0%; Pred. No. 4.8e-85;
Matches 351; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
PASCCHI1"
ACDSSSPSPASAA PRGAELVQSLVSLGSGLOHAKYLLIDPOKALFSSVKOE
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1144 AACCAAGAGTATACCATATTCACAGGACATATCTCTGCTGGAAGAGATCTGAG 1203
301 AGAAAGCAAGAGAGAAATACAGACCATATTCAGGAGCGGCAATATCAAGGCCCA 360
1204 AGAAAGCAAGAGAGAAATACAGACCATATTCAGGAGCGGCAATATCAAGGCCCA 1263
361 GTTTAGGCACTCATGCGCAACCAAAATGATGATGCCCA 399
1264 GTTTAGGCACTCATGCGCAACCAAAATGATGATGCCCA 1302
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AC118087/c 248901 bp DNA linear HTG 19-NOV-2002
LOCUS Rattus norvegicus clone CH230-38M5, *** SEQUENCING IN PROGRESS ***
DEFINITION 3 unordered pieces.
AC118087
VERSION 1
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 248901)
Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buha, C., Burch, P., Burrell, K., Caesar, H., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyne, M., Gree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Bayes, K., Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hu, Y., Hu, Y., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

TITLE Direct Submession
JOURNAL Unpublished
REFERENCE 2 (baees 1 to 143034)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
JOURNAL Direct Submession
TITLE Submitted (06-DEC-2001) Genome Center, University of Washington
REFERENCE Submitted (06-DEC-2001) Genome Center, University of Washington
AUTHORS Box 352145, Seattle, WA 98195, USA
TITLE 3 (baees 1 to 143034)
JOURNAL Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Senechimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
REFERENCE Direct Submession
AUTHORS Submitted (23-MAR-2002) Genome Center, University of Washington
JOURNAL Box 352145, Seattle, WA 98195, USA
TITLE On Mar 23, 2002 this sequence version replaced gi:17386316.

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Best Local Similarity 93.6%; Pred. No. 4.7e-52;
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DB 64035 TGTGTCATACAAAATCTCTCGAAGAGAGCAACAGCATTCAGCGCATGTGCT 64094
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RESULT 13
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DEFINITION Homo sapiens chromosome 5 clone RP11-1026L22, WORKING DRAFT
SEQUENCE 5 unordered pieces.
AC138808
AC138808.1 GI:27805220
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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REFERENCE 1 (bases 1 to 186485)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 186485)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1688774
Center clone name: RP11-11_1026L22
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Summary Statistics
Consensus quality: 182487 bases at least Q40
Consensus quality: 183346 bases at least Q30
Consensus quality: 183866 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 186085; sum-of-ctgigs estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 8.84 in Q20 bases; sum-of-ctgigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1126: contig of 1126 bp in length
* 1127 1226: gap of unknown length
* 1227 2350: contig of 1124 bp in length
* 2351 2450: gap of unknown length
* 2451 3522: contig of 1072 bp in length
* 3523 3622: gap of unknown length
* 3623 11173: contig of 7551 bp in length
* 11174 11273: gap of unknown length
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ORIGIN
Query Match 53.0%; Score 212; DB 2; Length 186485;
Best Local Similarity 93.6%; Pred. No. 4.7e-52;
Matches 221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 19 CCTAATACACGGATGCTACAGAGATCCCAAGAGAGGCTTTTGAAGAATTGA 78
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DB 132416 AATATCTCTTGCTTCAGGAGTGAACCTTCAACGATGATCAAGATTAATATTCCTT 132357
QY 139 TGTGTCATACAAAATCTCTCGAAGAGAGCAACAGCATTCAGCGCATGTGCT 198
DB 132356 TGTGTCATACAAAATCTCTCGAAGAGAGCAACAGCATTCAGCGCATGTGCT 132297
QY 199 TGGGACATAGCGGATCGAGACGCCATTGTAGAAGCCCTGAAACCAACAGGTATA 254
DB 132296 TGGGACATAGCGGATCGAGACGCCATTGTAGAAGCCCTGAAACCAACAGGTATA 132241
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RESULT 14
LOCUS AC143769 160170 bp DNA linear HTG 09-APR-2003
DEFINITION Macaca mulatta clone CH250-270D6, *** SEQUENCING IN PROGRESS ***
AC143769
AC143769.1 GI:29649247
VERSION HTG, HTGS PHASE2, HTGS_PGI.
KEYWORDS Macaca mulatta (rhesc-monkey)
SOURCE Macaca mulatta
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
1 (bases 1 to 160170)
Ceurows,M. and Mlosoavljevic,A.
Pooled genomic indexing (PGI): mathematical analysis and experiment design
(in) Gulgo, R. and Gusfield, D. (eds.);
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI 2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28; Springer (2002)
2 (bases 1 to 160170)
Mlosoavljevic,A., Sodergren,E., Ceurows,M., Li,B., Jackson,A.R., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Albrooks,S.L., Amarunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbarta,J., Benton,U., Bimaga,K., Blankenburg,K., Bonnin,D., Boucek,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhaq,C., Burch,P., Burrell,C., Burrell,K.L., Byrd,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavoules,C., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Demu,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.U., Draper,H., Dugan-Rocha,S., Durbin,K.J., Egan,A., Eshwar,C., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,J., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guerra,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homel,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korah,J., Kovar,C., Kravic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,D., Liu,W., Louleghed,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapa,P., Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Mercher,S., Metzger,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Monabdat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Norkenkw,S., Oguh,M., Okunou,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peary,J., Perez,L., Peters,L., Pickens,R., Priemu,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojudoan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., She,H., Shink,C., Shoohtari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Taneey,J., Taylor,C., Taylor,T., Telleria,B., Thomas,N., Thomas,S., Usmani,K., Vaequez,L., Vera,V., Vallon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Zucherlapati,R., Weinstein,G. and Gibbs,R.
Unpublished
3 (bases 1 to 160170)
Direct Submission
Worley,K.C.
Submitted (09-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: LASO
Center clone name: CH250-270D6
----- Summary Statistics
Chemistry: Dye-primer Bodipy: inf% of reads
Chemistry: Dye-terminator Big Dye: inf% of reads
Consensus quality: 9954 bases at least Q40
Consensus quality: 11529 bases at least Q30
Consensus quality: 13142 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: The contigs are based on the application
* of the PGI method using the Human genome (NCBI build 31)
* as the comparative genome.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 160170: contig of 160170 bp in length.
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CONFIDENCE: 0.83

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Best Local Similarity 98.6%; Pred. No. 6.5e-51;
Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 15
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DEFINITION Mus musculus chromosome 9, clone RP24-23JF22, complete sequence.
AC121264
AC121264.8 GI:46360003
VERSION HTG.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathii; Muridae; Murinae; Mus.
1 (bases 1 to 194261)

AUTHORS Birren,B., Nusbaum,C. and Lander,E.
 TITLE Mus musculus chromosome 9, clone RP24-233P22
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 194261)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
 Anderson,S., Barna,N., Baetien,V., Bloom,T., Boguslavsky,L.,
 Boukhalter,B., Brown,A., Camarata,J., Campoliano,A., Chang,U.,
 Chazaro,G., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
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 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (16-MAY-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 194261)
 JOURNAL
 REFERENCE
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,M., Arachchi,H.M., Barna,N., Baetien,V., Bloom,T.,
 Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
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 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Fero,S.,
 Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
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 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (11-MAR-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 194261)
 JOURNAL
 REFERENCE
 AUTHORS

TITLE Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
 Zimmer,A. and Zody,M.
 JOURNAL Direct Submission
 COMMENT Submitted (13-APR-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 13, 2004 this sequence version replaced gi:45356220.
 All repeats were identified using RepeatMasker:
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 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@road.mit.edu
 ----- Project Information
 Center project name: L21224
 Center clone name: 233_F_22

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Db	33370	AAGCCACCCCTTGGCTTCAGGAGATGAGACCCATCAACGACCAAGATTAACATTCGCCCT	33329
QY	139	TGTCGTATTAACAAAATCTCTCGGAAAGAGAGCAACAAGATCATTTCAAGCGCATTTGGTGT	198
Db	33330	GTGTCTCTACAGAACTCTTCGAGGAAGAGCAACAAGATCATTCGAGCGCATTTGGTGT	33389
QY	199	TGGGAGCATNAGCGGATCGAGACGGCATTTGTAGAAGCCCTGGAAACAACAGATTAACCA	258
Db	33390	CGGGAGCATGCGGAGCCGAGACGGCATTTGTAGAAGTGTGAGAGCCCTTGAGACATCTTAAG	33449
QY	259	TATTCACA	265
Db	33450	GCTCACA	33456

Search completed: January 31, 2005, 16:38:33
Job time : 2231.25 BECS

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 09:45:33 ; Search time 2037.02 Seconds
(without alignments)
8496.727 Million cell updates/sec

Title: US-09-996-630A-11_COPY_3800_4165

Perfect score: 366 1 cccttaacctgtcttcaaaa.....acatattgtcttcagcaat 366

Sequence: 1

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	100.0	1641	AK026013	AK026013 Homo sapi
2	366	100.0	3361	AK025449	AK025449 Homo sapi
3	366	100.0	4165	AX329586	AX329586 Sequence
4	366	100.0	4882	HUMK1A0	DA3636 Human mRNA
5	366	100.0	5140	BC071567	BC071567 Human mRNA
6	366	100.0	5519	AF226044	AF226044 Homo sapi
7	366	100.0	143034	AC104184	AC104184 Homo sapi
8	366	100.0	186485	AC138808	AC138808 Homo sapi
9	358	97.8	2580	G07259	G07259 human STR
10	300	82.0	396	AX337742	AX337742 Sequence
11	300	40.9	253055	AX409056	AX409056 Sequence
12	149.6	40.9	253055	AC106612	AC106612 Rattus no
13	132.2	36.1	4708	AF387809	AF387809 Mus muscu
14	132.2	36.1	162162	AL672224	AL672224 Mouse DNA
15	132.2	36.1	194261	AC121264	AC121264 Mus muscu
16	132.2	36.0	206641	AC120394	AC120394 Mus muscu
17	131.8	36.0	304	AX186951	AX186951 Sequence
18	120.8	33.0	329	AX185525	AX185525 Sequence
19	102.4	28.0	233777	AC100043	AC100043 Mus muscu

C 20	92.8	25.4	223685	2	AC122946	AC122946 Rattus no
C 21	86.6	23.7	232882	2	AC128448	AC128448 Rattus no
C 22	86.6	23.7	235834	2	AC116061	AC116061 Rattus no
C 23	86	23.5	199646	10	AC122264	AC122264 Mus muscu
C 24	75.2	20.5	106	6	C0657670	C0657670 Sequence
C 25	71.4	19.5	248901	2	AC118087	AC118087 Rattus no
C 26	67	18.3	489	6	AX371257	AX371257 Sequence
C 27	54	14.8	250743	3	AE014836	AE014836 Plasmodu
C 28	53.8	14.7	159109	2	CR376766	CR376766 Dario rer
C 29	53.8	14.7	179354	2	CR354588	CR354588 Dario rer
C 30	53	14.5	119181	5	BX005340	BX005340 Zebrafish
C 31	52.8	14.4	167868	10	AC116399	AC116399 Mus muscu
C 32	52.4	14.3	148465	5	AL772396	AL772396 Zebrafish
C 33	52.2	14.3	138655	2	CR391982	CR391982 Dario rer
C 34	52.2	14.3	150941	2	BX957281	BX957281 Dario rer
C 35	51.6	14.1	181789	5	BX321894	BX321894 Zebrafish
C 36	51.4	14.0	14635	3	AE001423	AE001423 Plasmodu
C 37	51.4	14.0	110096	2	CR388024	CR388024 Dario rer
C 38	51.2	14.0	110096	2	PFMAL13_00	PFMAL13_00 Plasmodu
C 39	51.2	14.0	110000	2	PFMAL13_01	PFMAL13_01 Plasmodu
C 40	51.2	14.0	192581	2	PFMAL13P1	PFMAL13P1 Plasmodu
C 41	51.2	13.9	126293	2	AC131747	AC131747 Homo sapi
C 42	51	13.9	126574	2	AP002018	AP002018 Homo sapi
C 43	51	13.9	162996	9	AC006441	AC006441 Homo sapi
C 44	51	13.9	164570	5	BX005280	BX005280 Zebrafish
C 45	51	13.9	169650	2	AC024629	AC024629 Homo sapi

ALIGNMENTS

RESULT 1
AK026013
LOCUS
AK026013 Homo sapiens cDNA: FLJ22360 fls, clone HRC06511.
DEFINITION
AK026013 GI:10438715
ACCESSION
AK026013
VERSION
AK026013.1
KEYWORDS
Oligo capping; fls (full insert sequence).
SOURCE
Homo sapiens
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
1
Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Oiyashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.

TITLE
JOURNAL
REFERENCE
AUTHORS
1
Unpublished
2 (bases 1 to 1641)

TITLE
JOURNAL
REFERENCE
AUTHORS
1
Submitted (29-APR-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)

COMMENT
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES
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/note="Cloning vector pME18SFL3"


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Db      3920   AATCTATCTGTATTTAAAGATGTGCACAATCTTGACACCATAATTTTAAAGATAGCTGTGAG    3979
QY      181   ACCGAATTTAAGATATATCCCTAACCAAGTGAAAATGATGTGTGTTTAAAGGGTACAGAAT    240
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QY      241   TATCAACTGATTTGGTCAGTGGCTGCCAATGCTGGTTGATTTCCCTCATTTGTGTAAACAT    300
Db      4040   TATCAACTGATTTGGTCAGTGGCTGCCAATGCTGGTTGATTTCCCTCATTTGTGTAAACAT    4099
QY      301   TGACAGCATGTATGACCAATGGGAAAAAAAATTCCAATATATATAAGCATATTTGGTGTTC    360
Db      4100   TGACAGCATGTATGACCAATGGGAAAAAAAATTCCAATATATATAAGCATATTTGGTGTTC    4155
QY      361   AGCAAT 366
Db      4160   AGCAAT 4165

RESULT 4
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LOCUS          HUNKIAAQ      4882 bp      mRNA      linear      PRI 10-MAY-2002
DEFINITION     Human mRNA for KIAA0096 gene, partial cds.
ACCESSION      D43636
VERSION        D43636.2 GI:20521877
KEYWORDS       KIAA0096.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS        Nagase,T., Miyajima,N., Tanaka,A., Sazuka,T., Seki,N., Sato,S.,
               Tabata,S., Ishikawa,K.-I., Kawarabayashi,Y., Kocani,H. and Nomura,N.'S.
               Prediction of the coding sequences of unidentified human genes.
               III. The coding sequences of 40 new genes (KIAA0081-KIAA0120)
               deduced by analysis of cDNA clones from human cell line KG-1
               DNA Res. 2 (1993) 37-43 (1993)

JOURNAL        JOURNAL
MEDLINE        95308325
PUBMED         7788527
REFERENCE      Chara,O., Nagase,T., Kikuno,R. and Nomura,N.
AUTHORS        Direct Submission
TITLE          Submitted (24-NOV-1994) Otsumu Ohara, Kazusa DNA Research Institute;
               1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
               (E-mail:kdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
COMMENT        On May 9, 2002 this sequence version replaced gi:598557.
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                /tissue_type="brain"
                /clone_lib="pbiscreptii SK plus"
                /note="This sequence was obtained by subcloning of the DNMA
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                /gene="KIAA0096"
                <1..2302
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[illegible]

ABRAMSON, R.D., MULLAHY, S.J., BOSEK, S.A., MCGHEE, P.J.,
MCKENNA, K.J., MALEK, J.A., GUNARATNE, P.H., RICHARDS, S.,
MORLEY, K.C., HALE, S., GARCIA, A.M., GAY, L.J., HULYK, S.W.,
VILLALON, D.K., MUZYNY, D.M., SODERGREN, E.J., LU, X., GIBBE, R.A.,
PANEY, J., HEITON, E., KETEMAN, M., MADAN, A., RODRIGUES, S.,
SANCHEZ, A., WHILING, M., MADAN, A., YOUNG, A.C., SHEVCHENKO, Y.,
BOUFFARD, G.G., BLAKESLEY, R.W., TOUCHMAN, J.W., GREEN, E.D.,
DICKSON, M.C., RODRIGUES, A.C., GRIMWOOD, J., SCHMUTZ, J., MYERS, R.M.,
BUTTERFIELD, Y.S., KRZYWINSKI, M.I., SKALSKA, U., SMALLIS, D.E.,
SCHERCH, A., SCHEIN, J.E., JONES, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 5140)
Strausberg, R.
Direct Submission
Submitted (01-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapdb-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-bhgsc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
Series: IRAK Plate: 167 Row: b Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21361642.
Location/Qualifiers

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FSNKPQPKLTTSCGSLAVSAEILIGDYDPAVDIVSLGVLFLMVCQGPPEA
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ORIGIN
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Query Match 100.0%; Score 366; DB 9; Length 5140;
Best Local Similarity 100.0%; Pred. No. 1.4e-64;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTTAACTGCTCTCAAAAGTGCATATAGTACAGTGTATTAATTAATTTATG 60
DB 4759 CCTTTAACTGCTCTCAAAAGTGCATATAGTACAGTGTATTAATTAATTTATG 4818
QY 61 GAAAAACAGTCTGTATTTTCTGTATGTGTATATATATATATATATATGACTTGC 120
DB 4819 GAAAAACAGTCTGTATTTTCTGTATGTGTATATATATATATATATATGACTTGC 4878
QY 121 AATTCTATCTGTATTTAAAGATGTGCAATCTTGACCAATTTTAAAGATAGCTGAG 180
DB 4879 AATTCTATCTGTATTTAAAGATGTGCAATCTTGACCAATTTTAAAGATAGCTGAG 4938
QY 181 ACCGAATTAAAGATATACCTACCAAGTAAATTTGATGTGTTAAGGGGTACGAAT 240
DB 4939 ACCGAATTAAAGATATACCTACCAAGTAAATTTGATGTGTTAAGGGGTACGAAT 4998
QY 241 TATCAACTGATTGTGTCAGTGTCTTCCATGCTGTGTTATTCCTCATTTGTATAACAT 300
DB 4999 TATCAACTGATTGTGTCAGTGTCTTCCATGCTGTGTTATTCCTCATTTGTATAACAT 5058
QY 301 TGAAGATATGTGACCAATGGGAAAAAATCCAAATTAATTAAGTACATTTGTGTTTC 360
DB 5059 TGAAGATATGTGACCAATGGGAAAAAATCCAAATTAATTAAGTACATTTGTGTTTC 5118
QY 361 AGCAAT 366
DB 5119 AGCAAT 5124

RESULT 6
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LOCUS Homo sapiens HSNFRK (HSNFRK) mRNA, complete cde.
DEFINITION AF226044
ACCESSION AF226044
VERSION AF226044.1 GI:9295326
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5519)
AUTHORS Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.
TITLE A novel gene expressed in human adrenal gland
JOURNAL Unpublished
2 (bases 1 to 5519)
REFERENCE Direct Submission
AUTHORS Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.
TITLE Submitted (19-JAN-2000) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, P. R. China
JOURNAL Location/Qualifiers

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LSRLKNIASPGTVHRRKRSQGRSSGSSSTDDSDSRRRLDKDGFYSWR
RCSGSPSGSGDGGQSKPSNAGVDKASPSNNAGGSGSGSGNPTVSGTR
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ORIGIN
Query Match 100.0%; Score 366; DB 9; Length 5519;
Best Local Similarity 100.0%; Pred. No. 1,3e-64;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTTAACCTGTCTTCAAAAGTTGCATCTAGTACAGTAGTGCTTAATTAATTGTG 60
Dy 5154 CCCTTAACCTGTCTTCAAAAGTTGCATCTAGTACAGTAGTGCTTAATTAATTGTG 5213
Qy 61 GAAAAAGCTGTGATTTTCTGATGTGTGATATATATATATATATATATATATATATAT 120
Dy 5214 GAAAAAGCTGTGATTTTCTGATGTGTGATATATATATATATATATATATATATATAT 5273
Qy 121 AATTCATCTGTATTTTAAAGATGTGACATCTTGACACCAATTTTAAAGATAGCTGTGAG 180
Dy 5274 AATTCATCTGTATTTTAAAGATGTGACATCTTGACACCAATTTTAAAGATAGCTGTGAG 5333
Qy 181 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATTTGATGTGTAGAGGGTACAGAT 240
Dy 5334 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATTTGATGTGTAGAGGGTACAGAT 5393
Qy 241 TATCACTGATTTGTGCTGCTGCTTCCAAATCTGCTGATTTCCCTCATTTGTGAACAT 300
Dy 5394 TATCACTGATTTGTGCTGCTGCTTCCAAATCTGCTGATTTCCCTCATTTGTGAACAT 5453
Qy 301 TGACAGGTATGTGACAAATGGAAAAAATCCAAATTAATTAAGTGAATATTTGCTGTC 360
Dy 5454 TGACAGGTATGTGACAAATGGAAAAAATCCAAATTAATTAAGTGAATATTTGCTGTC 5513
Qy 361 AGCAAT 366
Dy 5514 AGCAAT 5519
RESULT 7
AC104184 143034 bp DNA linear PRI 23-MAR-2002
LOCUS Homo sapiens chromosome 3 clone RP11-188P20, complete sequence.
DEFINITION AC104184 AC027581
AC104184.2 GI:19697457
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 143034)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 2 (bases 1 to 143034)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission

JOURNAL
COMMENT
Submitted (23-MAR-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Mar 23, 2002 this sequence version replaced gi:17386316.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Contact: uwgchgsen@u.washington.edu
Web site: http://www.genome.washington.edu
Drafting Center: BCM
----- Project Information
Center project name: chr-3
Center clone name: RP11-188P20 (bc0291)
----- Summary Statistics
Sequencing vector: Unknown; 58% of reads
Sequencing vector: plasmid; 108752; 42% of reads
Chemistry: Dye-terminator Big Dye; 67% of reads
Chemistry: Dye-terminator Big Dye; 33% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 142918 bases at least Q40
Consensus quality: 143028 bases at least Q30
Consensus quality: 143034 bases at least Q20
Insert size: 142838; sum-of-contigs
Quality coverage: 8.0x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5 : Mapping in progress
3 : RP11-258N2 (UWGC:bc0637) AC024378

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

BAC01 HindIII BglII
SeqDerMap FngRPrint SeqDerMap FngRPrint SeqDerMap FngRPrint

8696 8704 1129 1114 10270 10243

6 <800 6382 6515 2067 2063

2882 2945 512 <800 5480 5668

2540 2530 449 <800 3606 3574

3643 3781 2552 2517 928 930

1514	1486	3416	3369	365	<800
631	<800	7168	7307	7579	7709
865	847	1854	1889	782	<800
2055	2049	1636	1655	4596	4559
909	897	397	<800	2776	2784
3796	3781	2926	2977	184	<800
5481	5462	4712	4619	2132	2156
1935	1951	45	<800	856	867
507	<800	825	895	659	<800
120	<800	5281	5260	1899	1874
1153	1139	4614	4619	1261	1259
2841	2663	2273	2249	2817	2784
2145	2184	2075	2065	6712	6648
1526	1486	14383	14415	128	<800
1000	997	10039	9940	4209	4192
1126	1139	8620	8673	46	<800
1649	1651	501	<800	2157	2156
637	<800	11469	11355	6593	6648
788	<800	1883	1889	6080	6248
18870	19027	4982	4848	3363	3421
1312	1314	1943	1889	5134	5104
172	<800	886	895	5754	5668
3598	3303	881	895	4281	4192
1332	1314	85	<800	4197	4192
5599	5917	4281	4178	3177	3210
10560	10431	593	<800	9088	9070
7179	7208	66	<800	150	<800
3985	4046	3551	3581	2704	2784
9799	9561	488	<800	3282	3210
4653	4680	5651	5589	708	<800
1150	1139	2443	2517	8040	8083
7764	7701	1249	1229	3827	3766
5866	5917	4839	4848	228	<800
1182	1139	1244	1229	662	<800
1154	1139	185	<800	4221	4192
973	997	1386	1353	9761	9678
2345	2368	2602	2517	1167	1161

[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 186485)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 186485)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1688774
Center clone name: RPCI-11_1026L22

Summary Statistics
Consensus quality: 182487 bases at least Q40
Consensus quality: 183346 bases at least Q30
Consensus quality: 183866 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 186085; sum-of-contigs estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 8.84 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
* 1 1126: contig of 1126 bp in length
* 1127 1226: gap of unknown length
* 1227 2350: contig of 1124 bp in length
* 2351 2450: gap of unknown length
* 2451 3522: contig of 1072 bp in length
* 3523 3623: gap of unknown length
* 3623 11173: contig of 7551 bp in length
* 11174 11273: gap of unknown length
* 11274 186485: contig of 175212 bp in length.
Location/Qualifiers
1. 186485
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-1026L22"
/clone_1fb="RPCI human BAC library 11"

ORIGIN

Query Match 100.0%; Score 366; DB 2; Length 186485;
Best Local Similarity 100.0%; Pred. No. 6.7e-65;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTTAACCTGCTTCAAAAGTTCATATAGTACAGTAGTATAATTAATTAATTTGTG 60
DB 121990 CCCTTAACCTGCTTCAAAAGTTCATATAGTACAGTAGTATAATTAATTTGTG 121931
QY 61 GAAAAACAGCTTGTATTTTCTGTATGTGTATATATATATATATATATATATGACTTGGC 120
DB 121930 GAAAAACAGCTTGTATTTTCTGTATGTGTATATATATATATATATATATGACTTGGC 121871
QY 121 AATCTATCTGTATTTAAAGTGTGACAACTTGAACCACTTTTAAAGAAAGCTGTAG 180
DB 121870 AATCTATCTGTATTTAAAGTGTGACAACTTGAACCACTTTTAAAGAAAGCTGTAG 121811
QY 181 ACCGATTTAAAGATATCCCTACCAAGTGAATAATTTAGTGTGTTAAGAGGCTACAGAT 240
DB 121810 ACCGATTTAAAGATATCCCTACCAAGTGAATAATTTAGTGTGTTAAGAGGCTACAGAT 121751

QY 241 TATCACTGATTTGTCAGTGTGCTTCCAAATGCTGTGATTTCCATATGTTGAACAT 300
DB 121750 TATCACTGATTTGTCAGTGTGCTTCCAAATGCTGTGATTTCCATATGTTGAACAT 121691
QY 301 TGACAGTATGTGACAAATGGAAAAAATCCAAATTAATTAAGTGCATATTTGTTTC 360
DB 121690 TGACAGTATGTGACAAATGGAAAAAATCCAAATTAATTAAGTGCATATTTGTTTC 121631
QY 361 AGCAAT 366
DB 121630 AGCAAT 121625

RESULT 9

G07259 2580 bp DNA linear STS 19-OCT-1995
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 2580)
Hudson, T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: GTGATTATGATAGCTTGGAATGG
Primer B: AATGGTCAACACTGCTGATCC
STS size: 121
PCR Profile:

Presoak:

Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35

Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Prepared with primer pairs derived from D43636 -- Unigene.

FEATURES

Location/Qualifiers
1. 2580
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="764_B_9; 792_D_7; 817_D_5; 882_B_5; 897_F_7;
946_B_4; 959_B_2; 738_F_11"
1871. 1891
1871. 1895
complement(1971. 1991)

ORIGIN

Query Match 97.8%; Score 358; DB 11; Length 2580;

Best Local Similarity 97.8%; Pred. No. 6.5e-63;

Matches 358; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCTTAACTGCTTCAAAAGTTGATATAGTACAGTGTATATAATTAATTTG 60
DB 2215 CCTTAACTGCTTCAAAAGTTGATATAGTACAGTGTATATAATTTG 2274
QY 61 GAAAAACAGCTCTGATATTTCTGATATGTGTATATATATTAATTTG 120
DB 2275 GAAAAACAGCTCTGATATTTCTGATATGTGTATATATATTAATTTG 2334
QY 121 AATTCTATCTGATTTAAAGATGTGACCAATCTGACCAATTTAAGATTTAG 180
DB 2335 AATTCTATCTGATTTAAAGATGTGACCAATCTGACCAATTTAAGATTTAG 2394
QY 181 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATGATGTGTAAAGGTTACAG 240
DB 2395 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATGATGTGTAAAGGTTACAG 2454
QY 241 TATCAACTGATTTGTCAGTGTCTTCCATGCTGTTGATTTCCCTCATTTGTTAA 300
DB 2455 TATCAACTGATTTGTCAGTGTCTTCCATGCTGTTGATTTCCCTCATTTGTTAA 2514
QY 301 TGACAGTATGTGACAAATGGGAAAAAATCCAAATTAATTAAGTACATTTGTTG 360
DB 2515 TGACAGTATGTGACAAATGGGAAAAAATCCAAATTAATTAAGTACATTTGTTG 2574
QY 361 AGCAAT 366
DB 2575 AGCAAT 2580

RESULT 10
AX337742/c 396 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 8251 from Patent WO0194629.
DEFINITION AX337742
ACCESSION AX337742
VERSION AX337742.1 GI:18128461
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL Patent: WO 0194629-A 8251 13-DEC-2001;
Avalon Pharmaceuticals (US)

FEATURES
source 1. .396
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 82.0%; Score 300; DB 6; Length 396;

Best Local Similarity 91.0%; Pred. No. 5.3e-51;

Matches 333; Conservative 17; Mismatches 13; Indels 3; Gaps 3;

QY 1 CCTTAACTGCTTCAAAAGTTGATATAGTACAGTGTATATAATTTG 60
DB 363 CCTTAACTGCTTCAAAAGTTGATATAGTACAGTGTATATAATTTG 304
QY 61 GAAAAACAGCTCTGATATTTCTGATATGTGTATATATTAATTTG 120
DB 303 G-GAAACAGCTCTGATATTTCTGATATGTGTATATTAATTTG 245
QY 121 AATTCTATCTGATTTAAAGATGTGACCAATCTGACCAATTTAAGATTTAG 180

DB 244 AADTCATCTGATTTAAAGATGTGACCAATTTAAGATTTAGCTGTG 185
QY 181 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATGATGTGTAAAGGTTACAG 240
DB 184 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATGATGTGTAAAGGTTACAG 126
QY 241 TATCAACTGATTTGTCAGTGTCTTCCATGCTGTTGATTTCCCTCATTTGTTAA 300
DB 125 TATCAACTGATTTGTCAGTGTCTTCCATGCTGTTGATTTCCCTCATTTGTTAA 67
QY 301 TGACAGTATGTGACAAATGGGAAAAAATCCAAATTAATTAAGTACATTTGTTG 360
DB 66 TGACAGTATGTGACAAATGGGAAAAAATCCAAATTAATTAAGTACATTTGTTG 7
QY 361 AGCAAT 366
DB 6 AGCAAT 1

RESULT 11
AX409056/c 396 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 1703 from Patent WO0229103.
DEFINITION AX409056
ACCESSION AX409056
VERSION AX409056.1 GI:21441761
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Alvarez, C., Horne, D., Perez-da-Silva, S. and Vockley, J. G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 1703 11-APR-2002;
GENE LOGIC INC (US)

FEATURES
source 1. .396
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="EMBL/Genbank Accession No. D60769"

ORIGIN

Query Match 82.0%; Score 300; DB 6; Length 396;

Best Local Similarity 91.0%; Pred. No. 5.3e-51;

Matches 333; Conservative 17; Mismatches 13; Indels 3; Gaps 3;

QY 1 CCTTAACTGCTTCAAAAGTTGATATAGTACAGTGTATATAATTTG 60
DB 363 CCTTAACTGCTTCAAAAGTTGATATAGTACAGTGTATATAATTTG 304
QY 61 GAAAAACAGCTCTGATATTTCTGATATGTGTATATATTAATTTG 120
DB 303 G-GAAACAGCTCTGATATTTCTGATATGTGTATATTAATTTG 245
QY 121 AATTCTATCTGATTTAAAGATGTGACCAATCTGACCAATTTAAGATTTAG 180
DB 244 AADTCATCTGATTTAAAGATGTGACCAATTTAAGATTTAGCTGTG 185
QY 181 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATGATGTGTAAAGGTTACAG 240
DB 184 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATGATGTGTAAAGGTTACAG 126
QY 241 TATCAACTGATTTGTCAGTGTCTTCCATGCTGTTGATTTCCCTCATTTGTTAA 300
DB 125 TATCAACTGATTTGTCAGTGTCTTCCATGCTGTTGATTTCCCTCATTTGTTAA 67
QY 301 TGACAGTATGTGACAAATGGGAAAAAATCCAAATTAATTAAGTACATTTGTTG 360
DB 66 TGACAGTATGTGACAAATGGGAAAAAATCCAAATTAATTAAGTACATTTGTTG 7
QY 361 AGCAAT 366

Db 6 AGCATT 1

RESULT 12
AC106612/c
LOCUS
DEFINITION
AC106612 252055 bp DNA linear HTG 13-MAY-2003
*** 6 unordered pieces. *** SEQUENCING IN PROGRESS

ACCESSION
AC106612 GI:30579444
HTG: HTGS PHASE1: HTGS DRAFT: HTGS ENRICHED.
KEYWORDS
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus

REFERENCE
AUTHORS
1 (bases 1 to 252055)
Mizny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooke, S., Amin, A., Anguiano, D., Ayala-Becchi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, F., Bismail, K., Blair, D., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Devila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falle, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabis, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gatregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Healand, W., Hamli, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howell, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovac, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshuwa, L., Loulsged, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., McWhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mlosoavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokwelen, O., Okunnu, G., Olariunasegun, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pflannkuch, C., Plappert, P., Polidexter, A., Popovic, D., Primus, E., Pu, L.-L., Piazzi, M., Quiroz, J., Rachin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Saverly, G., Scherer, S., Scott, G., Shaceman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Slabson, I., Sitter, C.D., Snaiz, D., Steed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steelme, M., Strong, R., Sutton, A., Syatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemami, K., Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhou, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department

REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 252055)
Rat Genome Sequencing Consortium.

COMMENT

On May 13, 2003 this sequence version replaced gi:24819088. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GLRO
Center clone name: CH230-175A5
----- Summary Statistics

Assembly program: Atlas 3.0
Consensus quality: 216498 bases at least Q40
Consensus quality: 220368 bases at least Q30
Consensus quality: 223168 bases at least Q20
Estimated insert size: 230938; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 243681: contig of 243681 bp in length
* 243782 243781: gap of unknown length
* 243782 244985: contig of 1204 bp in length
* 244986 245085: gap of unknown length
* 245086 246426: contig of 1341 bp in length
* 246427 246526: gap of unknown length
* 246527 247527: contig of 1001 bp in length
* 247528 247627: gap of unknown length
* 247628 248934: contig of 1307 bp in length
* 248935 249034: gap of unknown length
* 249035 252055: contig of 3021 bp in length.

FEATURES

source

misc_feature

misc_feature

misc_feature

1. 252055
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-175A5"
1303. 1905
/note="clone boundary
clone end:Spf
site:EcORI
end_sequence: BH351404"
240925. 241490
/note="clone boundary
clone end:T7
site:EcORI

ORIGIN

end_sequence: BH551402"

Query Match 40.9%; Score 149.6; DB 2; Length 252055;
Best Local Similarity 76.2%; Pred. No. 4.2e-21;
Matches 279; Conservative 0; Mismatches 69; Indels 18; Gaps 7;

QY 1 CCCTTAACCTGCTGCAAAAGTGCATATAGTACAGTGTATTAATTAATTTG 60
DB 230496 CCCCTAACCTGCTTCCAGAAAGTGCATATAGTACAGTGTATTAATTAATTTG 230437
QY 61 GAAAAACAGCTCTGATTTTTCGTAATGTGTATATATATTAATTAATTTG 120
DB 230436 GGGAA--AGTTACTCTGTAATTTTTCGTAATGTGTATATATTAATTAATTTG 230380
QY 121 AATTCATCTGTATTAAGATGACAAATCTGACACCAATTTTAAGAACTACTGTG 180
DB 230379 AATTCATCTGTATTAAGATGACAAATCTGACACCAATTTTAAGAACTACTGTG 230327
QY 181 ACCGAATTAAGATTAATCCCTACCAAGTGAATAATGATGTGTAAAGAGGTACAAAT 240
DB 230326 TGAGCTGAACTAAGATGTGTAGAGAGTCAAGTTGTGTCT---GAGAGATACACT 230270
QY 241 TATCAACTGATTTGTCAGTTGCTTCCATGCTGTGTGATTTCCCTCATTTGTGAAACAT 300
DB 230269 TGTCAACCCGA-TTGTCAAGCTGCTCTAGT-CTGGCCAGCTTTTTCCTGTGTGAACAT 230212
QY 301 TGACAGTATGTGACAAATGGGAAAAAATCCAAATTAATTAAGTACATTTGCTTC 360
DB 230211 TGACAGTATGTGACAGATGGGAAATTA--TCTAATTAATTAAGTACATTTGCTTC 230155
QY 361 AGCAAT 366
DB 230154 AGCAAT 230149

RESULT 13
AF387809 4708 bp mRNA linear ROD 13-SEP-2002
LOCUS Mus musculus strain BALB/c SNF-1 related kinase (Snrk) mRNA,
DEFINITION complete cds.

ACCESSION AF387809
VERSION AF387809.2 GI:16418486
KEYWORDS

SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE 1 (bases 1 to 4708)
AUTHORS Kertesiz,N., Samson,J., Debacquer,C., Wu,H. and Labastie,M.-C.
TITLE Cloning and characterization of human and mouse SNRK sucrose
non-fermenting protein (SNF-1)-related kinases

JOURNAL Gene 294 (1-2), 13-24 (2002)
REFERENCE 2 (bases 1 to 4708)
AUTHORS Labastie,M.-C. and Samson,J.
TITLE Direct Submision

JOURNAL Submitted (01-JUN-2001) Institut d'Embryologie Cellulaire et
Moleculaire, CNRS et College de France, 49 bis, Ave. de la Belle
Gabrielle, Nogent Sur Marne 94130, France

REFERENCE 3 (bases 1 to 4708)
AUTHORS Labastie,M.-C. and Samson,J.
TITLE Direct Submision

JOURNAL Submitted (25-OCT-2001) Institut d'Embryologie Cellulaire et
Moleculaire, CNRS et College de France, 49 bis, Ave. de la Belle
Gabrielle, Nogent Sur Marne 94130, France

REMARK COMMENT Sequence update by submitter
On Oct 25, 2001 this sequence version replaced gi:15420742.
FEATURES Location/Qualifiers

1..4708
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"

/cissue_type="yolk sac"
/dev_stage="12.5 dpc"
1..4708
/gene="Snrk"
149..2395
/gene="Snrk"
/note="SNRK"
/codon_start=1
/product="SNF-1 related kinase"
/protein_id="AAK97440.1"
/db_xref="GI:15420743"

CDS

polyA_signal 4662..4667
/gene="Snrk"

ORIGIN

Query Match 36.1%; Score 132.2; DB 10; Length 4708;
Best Local Similarity 72.7%; Pred. No. 3.1e-17;
Matches 245; Conservative 0; Mismatches 73; Indels 19; Gaps 5;

QY 30 AGTTACAGTGTGTAATTAATTAATTTGTGAAAAACGCTGTGATTTTCTGATGT 89
DB 4373 AGTTACAGTGTGTAATTAATTAATTTGTGAAAAAGTGTGTTGATTTTC---TGT 4428
QY 90 GTGTATATATATATATATATATGACTTCTGCAATCTATCTGATTTTAAGATGACAA 149
DB 4429 GTGTATATATATATATATATATGACTTCTGCAATCTATCTGATTTTAAGATGACAA 1487
QY 150 TCTTGACACCAATTTTAAGATAGCTGTGAGACCAATTAAGATATTCCTACCAAGTG 209
DB 4488 TCTTGACACCAATTTTAA-----TAGTCATGAGCCTGGAACAAAGATGCTTACAG 4537
QY 210 AATATGATGTGTGTAAGAGGTACAGAAATATATACGATTTGTGCTGCTTCCCA 269
DB 4538 CCAAGTGTGTATGTGTGAGAACCAACTGTGAGCT-AATGTGTGATGCTGCTTACAG 4596
QY 270 TGTGTGTGATTTCCCTCATTTGTGTAACATTTGACAGATGATGACAAATGGAAGAAA 329
DB 4597 TTTGTACCAAGCTTTTTCCTTGTGTGACATTTGACAGATGATGACAAATGGAAGAAA 4655
QY 330 ATCCAAATTAATTAAGTACATATTTGTTTCAGCAAT 366
DB 4656 --TCCAAATTAATTAAGTACATATTTGTTTCAGCAAT 4690

RESULT 14

AL672224 162162 bp DNA linear ROD 29-AUG-2002
LOCUS Mouse DNA sequence from clone RP23-360B14 on chromosome X, complete
DEFINITION sequence.

ACCESSION AL672224
VERSION AL672224.15 GI:22552833
KEYWORDS

SOURCE HTG.
ORGANISM Mus musculus (house mouse)
MUS musculus

REFERENCE 1 (bases 1 to 162162)
AUTHORS Lovell,J.
TITLE Direct Submision

JOURNAL

Submitted (28-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 On Aug 30, 2002 this sequence request: clonerequest@sanger.ac.uk
 COMMENT ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emi, EMBL; Swi, SWISSPROT; Tr, TrEMBL; Wp, WormPep; Information on the WormPep database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-360B14 is from the RP23-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6

FEATURES

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 /clone="RP23-360B14"
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ORIGIN

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 Best Local Similarity 72.7%; Pred. No. 1.5e-17;
 Matches 245; Conservative 0; Mismatches 73; Indels 19; Gaps 5;
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 90 GTGATATATATATATATATGTTGGAAGAAACAGCTTGTATTTCTGTATGT 149
 Db 66506 GTGATATATATATATATATGTTGGAAGAAACAGCTTGTATTTCTGTATGT 149
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 150 TCTTGACACCAATTTTAAAGATAGCTGACGACCAATTAAGATTAATCCCTACCAAGT 209
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 270 TGTGCTGTTGATTTCCCTCATTTGTTGAACATTGACAGGATGTCACAAATGGGAAAAA 329
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RESULT 15
 AC121264

LOCUS AC121264 194261 bp DNA linear ROD 13-APR-2004
 DEFINITION Mus musculus chromosome 9, clone RP24-233F22, complete sequence.
 AC121264
 VERSION AC121264.8 GI:46360003
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Baran, N., Baatien, V., Bloom, T., Bogniavsky, L., Boukhgalter, B., Brown, A., Cantarel, J., Campagna, A., Chang, J., Chazaro, B., Choquet, Y., Collinge, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Labrecque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McSwan, P., McKernan, K., Meldrum, J., Menus, L., Minova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhphang, P., Pierce, N., Pollard, V., Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talmas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, D., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL Submitted (16-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 194261)

REFERENCE

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Baran, N., Baatien, V., Bloom, T., Bogniavsky, L., Boukhgalter, B., Cantarel, J., Chang, J., Choquet, Y., Chazaro, B., Choquet, Y., Collinge, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Labrecque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McSwan, P., McKernan, K., Meldrum, J., Menus, L., Minova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhphang, P., Pierce, N., Pollard, V., Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talmas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, D., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL Submitted (11-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 194261)

REFERENCE

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Baran, N., Baatien, V., Bloom, T., Bogniavsky, L., Boukhgalter, B., Cantarel, J., Chang, J., Choquet, Y., Chazaro, B., Choquet, Y., Collinge, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Labrecque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McSwan, P., McKernan, K., Meldrum, J., Menus, L., Minova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhphang, P., Pierce, N., Pollard, V., Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talmas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, D., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarty, M., McDermid, J., Meneus, L., Mihova, T., Mienna, Y., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Pinunhang, P., Pierre, N., Rachupka, A., Ramsamy, U., Raymond, C., Reita, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testa, S., Theodore, J., Topham, K., Travers, M., Vassiliou, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.

Direct Submission
Submitted (13-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 13, 2004 this sequence version replaced gi:45356220.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@prodd.mit.edu
----- Project Information
Center project name: L21224
Center clone name: 233_F_22

Some of the sequence contained within base pairs 175167 to the end of the clone was stolen from accession AC108846 [WIGR Project L21006].

FEATURES

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Query Match 36.1% Score 132.2; DB 10; Length 194261;

Best Local Similarity 72.7%; Pred. No. 1.5e-17; Indels 19; Gaps 5;

Matches 245; Conservative 0; Mismatches 73; Indels 19; Gaps 5;

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Tue Feb 1 09:08:45 2005

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Db 42551 --TCCAATTAATTAAGTGACATATTGTTGTCAGCAAT 42585

Search completed: January 31, 2005, 16:38:39
Job time : 2043.02 secs

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Db 2290 TGCTTCGTTTAAATAAAGTGCCCTGG 2317
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RESULT 2
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LOCUS BD272343
DEFINITION Methods of diagnosing or treating neurological diseases and cell
degeneration.
ACCESSION BD272343
VERSION BD272343.1 GI:33082111
KEYWORDS JP 2002530076-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS 1 (bases 1 to 4186)
TITLE Nitech,R. and Greeve,I.
METHODS Methods of diagnosing or treating neurological diseases and cell
degeneration
PATENT Patent: JP 2002530076-A 3 17-SEP-2002;
JOURNAL ROGER NITSCH, ISABELL, GREEVE
COMMENT OS Homo sapiens (human)
PN JP 2002530076-A/3
PD 17-SEP-2002 JP 2000582553
PF 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL, GREEVE
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
PC A61P11/00,A61P15/00,A61P21/00,A61P25/00,A61P25/14,A61P25/16,
PC A61P25/28,
PC A61P43/00,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10,C12Q1/PC
68',G01N33/53,G01N33/53,C12N15/00,C12N5/00,A61K37/02 CC Methods
of diagnosing or treating neurological diseases and CC
cell
CC degeneration
FT source
FT source

FEATURES
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1..4186
Location/Qualifiers
/organism="Homo sapiens"
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ORIGIN

Query Match 100.0%; Score 388; DB 6; Length 4186;
Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 4099 TACAGCCACAGGACCTGTGTCTACTGTCTGGAAGACATGTCCTCGTGTGGGCCCC 4158
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RESULT 3
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LOCUS AX026418
DEFINITION Sequence 4 from Patent EP1002862.
ACCESSION AX026418
VERSION AX026418.1 GI:10187648
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS 1
TITLE Methods of diagnosing or treating neurological diseases
JOURNAL NITSCH ROGER M PROF DR (DE)
PATENT Patent: EP 1002862-A 4 24-MAY-2000;
COMMENT Location/Qualifiers
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ORIGIN

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Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Page 3

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5-SEP-2000

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300

CTCT 4099

CCGC 360

CCGC 4159

-JAN-2002

ACCESSION AX334630
VERSION AX334630.1 GI:18125349
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL Patent: WO 0194629-A 5139 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 388; DB 6; Length 4187;
Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 3980 TGGATATTAAGTGAAGAGGAGGAGTGAAGTGGTGTGAGCACTATGATGATTTT 4039
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DB 4040 ATTTCTTTCTTTGTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4099
QY 301 TACAGCCACAGGACATGTCATCTCTGTCGAGACATGTCCTGCTGCTGGGCGCG 360
DB 4100 TACAGCCACAGGACATGTCATCTCTGTCGAGACATGTCCTGCTGCTGGGCGCG 4159
QY 361 TGGTCTGTTTAAATAAAGTGCCCTGG 388
DB 4160 TGGTCTGTTTAAATAAAGTGCCCTGG 4187
RESULT 7
AX408962 4187 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 1609 from Patent WO0229103.
DEFINITION AX408962
ACCESSION AX408962
VERSION AX408962.1 GI:21441667
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1
Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 1609 11-Apr-2002;
GENE LOGIC INC (US)
FEATURES
source 1. 4187
/organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. D13643"
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Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 3860 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGAGCTGCA 3919
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DB 3920 TGAAGTTTCTTTAGAAATCAGAAATGTGACCACTTTCTTGCCGAGAAAGATGAACT 3979
QY 181 TGGATATTAAGTGAAGAGGAGGAGTGAAGTGGTGTGAGCACTATGATGATTTT 240
DB 3980 TGGATATTAAGTGAAGAGGAGGAGTGAAGTGGTGTGAGCACTATGATGATTTT 4039
QY 241 ATTTCTTTCTTTGTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
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QY 301 TACAGCCACAGGACATGTCATCTCTGTCGAGACATGTCCTGCTGCTGGGCGCG 360
DB 4100 TACAGCCACAGGACATGTCATCTCTGTCGAGACATGTCCTGCTGCTGGGCGCG 4159
QY 361 TGGTCTGTTTAAATAAAGTGCCCTGG 388
DB 4160 TGGTCTGTTTAAATAAAGTGCCCTGG 4187
RESULT 8
AX828407 4187 bp DNA linear PAT 12-DEC-2003
LOCUS Sequence 53 from Patent WO03074073.
DEFINITION AX828407
ACCESSION AX828407
VERSION AX828407.1 GI:39838407
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Al-Mahmoud, S., Colin, S. and Schneider, C.
TITLE Genes involved in regulating angiogenesis, pharmaceutical
JOURNAL preparations containing same and applications thereof
Patent: WO 03074073-A 53 12-SEP-2003;
Gene Signal (PR)
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Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGAGCTGCA 120
DB 3860 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGAGCTGCA 3919

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 DB 3980 TGAATATTACTGAAGGAGGAGTGAAGATGGTGTGAGATGTATGTGTGATTTT 4039
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 QY 301 TACAGCCACAGGACCTGTCTACTGTCTGAAGACATGTCCCTGTGCTGTGGGCGCC 360
 DB 4100 TACAGCCACAGGACCTGTCTACTGTCTGAAGACATGTCCCTGTGCTGTGGGCGCC 4159
 QY 361 TGCTTCTGTTTAATAATAAGTGCGCTGG 388
 DB 4160 TGCTTCTGTTTAATAATAAGTGCGCTGG 4187

RESULT 9
 LOCUS HUMSC390 4187 bp mRNA linear PRI 06-OCT-2001
 DEFINITION Homo sapiens mRNA for KIAA0018 protein, partial cds.
 ACCESSION D13643
 VERSION D13643.2 GI:6630631
 KEYWORDS KIAA0018 protein.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1
 TITLE Numura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.
 Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1
 JOURNAL DNA RESEARCH 1(1), 27-35 (1994)
 MEDLINE 96051387
 PUBMED 7584026

REFERENCE
 AUTHORS 2
 TITLE Numura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.
 Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)
 JOURNAL DNA RESEARCH 1(1), 47-56 (1994)
 MEDLINE 96051389
 PUBMED 7584028

REFERENCE
 AUTHORS 3 (bases 1 to 4187)
 TITLE Ohara, O., Nagase, T., Kikuno, R. and Numura, N.
 Direct Submission
 Submitted (11-NOV-1992) Otsu Ohara, Kazuo DNA Research Institute;
 1332-3, Yana, Kisarazu, Chiba 292-0812, Japan
 E-mail: cdnainfo@kazuoka.or.jp, Tel: +81-438-52-3913
 On Dec 22, 1999 this sequence version replaced gi:265996.
 COMMENT Sequence updated (20-Dec-1999).
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 /gene="KIAA0018"
 <1. .1589
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 QY 181 TGAATATTACTGAAGGAGGAGTGAAGATGGTGTGAGATGTATGTGTGATTTT 240
 DB 3980 TGAATATTACTGAAGGAGGAGTGAAGATGGTGTGAGATGTATGTGTGATTTT 4039
 QY 241 ATTTTCTTTCTTTGTCATGGGGGCAAGAGAAAGCATGATCTTCCCTGTCAAGCTCT 300
 DB 4040 ATTTTCTTTCTTTGTCATGGGGGCAAGAGAAAGCATGATCTTCCCTGTCAAGCTCT 4099
 QY 301 TACAGCCACAGGACCTGTCTACTGTCTGAAGACATGTCCCTGTGCTGTGGGCGCC 360
 DB 4100 TACAGCCACAGGACCTGTCTACTGTCTGAAGACATGTCCCTGTGCTGTGGGCGCC 4159
 QY 361 TGCTTCTGTTTAATAATAAGTGCGCTGG 388
 DB 4160 TGCTTCTGTTTAATAATAAGTGCGCTGG 4187

RESULT 10
 LOCUS BC004375 4202 bp mRNA linear PRI 29-JUN-2004
 DEFINITION Homo sapiens 24-dehydrocholesterol reductase, mRNA (cDNA clone MGC:10563 IMAGE:3698639), complete cds.
 ACCESSION BC004375
 VERSION BC004375.1 GI:13325123
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 4202)
 TITLE Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

ORIGIN

Query Match 100.0%; Score 388; DB 9; Length 4187;
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 Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 NSDLFYAVPWSGCTIGFVAAERITIPAKVYLRPEPVGALCAKPFHESORON
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CC key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.2e-116; Mismatches 0; Indels 0; Gaps 0;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCATGTGAAAAGTATCAGATTAAGCTCTCCCTCCAGAGCCCTGAGTTTCTTGGCTGCA 120
DB 3921 GCATGTGAAAAGTATCAGATTAAGCTCTCCCTCCAGAGCCCTGAGTTTCTTGGCTGCA 3980

QY 121 TGAAGTTTCTTTAGATCAGAAATGTAGCCAGTTCTTGGCCAGAAAGATGAATACT 180
DB 3981 TGAAGTTTCTTTAGATCAGAAATGTAGCCAGTTCTTGGCCAGAAAGATGAATACT 4040

QY 181 TGAATATTACTGAAAAGGAGGGGTGAGATGGGTGTGGCAGTGAATAGTGTGATTTT 240
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DB 4101 ATTTTCTTTTGGTCAATGGGGCCAAAGAGAAAGCATGATCTTCCCTGTCAGGCTCT 4160

QY 301 TACAGCCACAGGCACTGTCTACTGTCTGGAAGACATGTCCTGGCTGTGGGGCCGC 360
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QY 361 TGCCTCTGTTTAATAAAGTGCCCTGG 388
DB 4221 TGCCTCTGTTTAATAAAGTGCCCTGG 4248

RESULT 12
CQ776643 4248 bp DNA linear PAT 11-MAR-2004
LOCUS Sequence 329 from Patent EP1394274.
ACCESSION CQ776643
VERSION CQ776643.1 GI:45380033
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
Patent: EP 1394274-A 329 03-MAR-2004;
Genex Research, Inc. (JP)
JOURNAL Location/Qualifiers
FEATURES
source 1..4248
/organism="Homo sapiens"
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ORIGIN
Query Match 100.0%; Score 388; DB 6; Length 4248;
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QY 61 GCATGTGAAAAGTATCAGATTAAGCTCTCCCTCCAGAGCCCTGAGTTTCTTGGCTGCA 120
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QY 121 TGAAGTTTCTTTAGATCAGAAATGTAGCCAGTTCTTGGCCAGAAAGATGAATACT 180
DB 3981 TGAAGTTTCTTTAGATCAGAAATGTAGCCAGTTCTTGGCCAGAAAGATGAATACT 4040

QY 181 TGAATATTACTGAAAAGGAGGGGTGAGATGGGTGTGGCAGTGAATAGTGTGATTTT 240
DB 4041 TGAATATTACTGAAAAGGAGGGGTGAGATGGGTGTGGCAGTGAATAGTGTGATTTT 4100

QY 241 ATTTTCTTTTGGTCAATGGGGCCAAAGAGAAAGCATGATCTTCCCTGTCAGGCTCT 300
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DB 4161 TACAGCCACAGGCACTGTCTACTGTCTGGAAGACATGTCCTGGCTGTGGGGCCGC 4220

QY 361 TGCCTCTGTTTAATAAAGTGCCCTGG 388
DB 4221 TGCCTCTGTTTAATAAAGTGCCCTGG 4248

RESULT 13
CQ776840 4248 bp DNA linear PAT 11-MAR-2004
LOCUS Sequence 526 from Patent EP1394274.
ACCESSION CQ776840
VERSION CQ776840.1 GI:45380230
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
Patent: EP 1394274-A 526 03-MAR-2004;
Genex Research, Inc. (JP)
JOURNAL Location/Qualifiers
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source 1..4248
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/db_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 9.2e-116; Mismatches 0; Indels 0; Gaps 0;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	TACAGCCACAGGCATCTGTCTACTGTGTGSAAGCATGTCCCGTGCCTGTGGGGCGCG	4220
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Db	TGCTTCTGTTTAAATAAAGTGGCTGG	4248

RESULT	14				
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LOCUS	AX026416	4248 bp	DNA	linear	PAT 16-SEP-2000
DEFINITION	Sequence 2 from Patent EP1002862.				
VERSION	AX026416				
VERSION	AX026416.1	GI:10187646			
KEYWORDS					
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				

REFERENCE	1
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
SOURCE	
	Methods of diagnosing or treating neurological diseases
	Patent: EP 1002862-A 2 24-MAY-2000;
	NITSCH ROGER M PROF DR (DE)
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OY	61	GCATGTGGAAAGTATCAGATGAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGAGTCGA	120
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OY	181	TGGATATTACTGAAAAGGGAGGGGTGGAGATGGGTGTGGCACTGTAATGTGTGATATTTT	240
Db	4041	TGGATATTACTGAAAAGGGAGGGGTGGAGATGGGTGTGGCACTGTAATGTGTGATATTTT	4100
OY	241	ATTTTCTCTTTGGTCATGGGAGGCCAAGAGAAAGGCATGATCTTCCCTTCAGGCTCT	300
Db	4101	ATTTTCTCTTTGGTCATGGGAGGCCAAGAGAAAGGCATGATCTTCCCTTCAGGCTCT	4160
OY	301	TACAGCCACAGGCACTGTGTTACTGTCTGGAAGACATGTCCCGTGGCTGTGGGGCCGC	360
Db	4161	TACAGCCACAGGCACTGTGTTACTGTCTGGAAGACATGTCCCGTGGCTGTGGGGCCGC	4220
OY	361	TGCTTCGTGTTAAATGAAGTGGCTGG 388	
Db	4221	TGCTTCGTGTTAAATGAAGTGGCTGG 4248	

RESULT 15			
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LOCUS	AX828386	4248 bp	DNA
DEFINITION	Sequence 32 from Patent WO03074073.	linear	PAT 12-DEC-2003

ACCESSION	AX8283386
VERSION	AX8283386.1
KEYWORDS	GI:398383386
SOURCE	.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Al-Mahmoud S., Collin S. and Schneider C.
TITLE	Genes involved in regulating angiogenesis, pharmaceutical
	preparations containing same and applications thereof
JOURNAL	Patent: WO 03074073-A 32 12-SEP-2003;
	Gene Signal (FR)
FEATURES	Location/Qualifiers
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Db	3921	GCAATGGAAGATATCAGATGAAGCCCTCCCTCCAGAGCCCTGATTTCTTGSGCTGCA	3980			
Qy	121	TGAAGTTTTCTTTAGATCAGAAATTGTAGCCAGTTTCTTTGGCCAAAGATGAATACT	180			
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Qy	181	TGATATTTACTGAAAGGGAGGGGTGGAGATGGGTGTGGCAGTGTATGTGTGATTTTT	240			
Db	4041	TGATATTTACTGAAAGGGAGGGGTGGAGATGGGTGTGGCAGTGTATGTGTGATTTTT	4100			
Qy	241	ATTTTCTTCTTTGGTCAATGGGGGCCAAGAGAAAGCATGAATCTTCCCTGTCAAGCTCT	300			
Db	4101	ATTTTCTTCTTTGGTCAATGGGGGCCAAGAGAAAGCATGAATCTTCCCTGTCAAGCTCT	4160			
Qy	301	TACAGCCACAGGCACTGTGTCTATCTGTCTGGAAGACATGTCCCGTGGCTGTGGGGCCG	360			
Db	4161	TACAGCCACAGGCACTGTGTCTATCTGTCTGGAAGACATGTCCCGTGGCTGTGGGGCCG	4220			
Qy	361	TGCTTCGTTTAAATAAAGTGGCCCTGG	388			
Db	4221	TGCTTCGTTTAAATAAAGTGGCCCTGG	4248			

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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SUMMARIES

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4	400	100.0	4187	AX026417	AX026417 Sequence
5	400	100.0	4187	AX334630	AX334630 Sequence
6	400	100.0	4187	AX408962	AX408962 Sequence
7	400	100.0	4187	AX828407	AX828407 Sequence
8	400	100.0	4187	HUMRSC390	D13643 Homo sapien
9	400	100.0	4248	BD272341	BD272341 Methods o
10	400	100.0	4248	CQ776643	CQ776643 Sequence
11	400	100.0	4248	CQ776840	CQ776840 Sequence
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	25	322	80.5	1557	6	AX814446
	26	284	71.0	728	6	BD083782
	27	284	71.0	728	6	BD097429
	28	284	71.0	4219	6	BD167659
	29	272.8	68.2	425	6	AF38936S1
	30	272.8	68.2	155925	9	AC096536
	31	272.8	68.2	169072	9	AC009946
	32	224.6	56.1	3994	10	BX511043
	33	224.6	56.1	246011	10	AL929585
	34	215	53.8	211500	2	AC117905
	35	215	53.8	262897	2	AC129688
	36	168.8	42.2	2012	5	BC078029
	37	167.2	41.8	1994	5	BC074393
	38	135	33.8	392	9	AF398336S2
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	40	109.2	27.3	180994	5	BX255909
	41	109.2	27.3	192688	2	BX511260
	42	109.2	27.3	213297	2	BX323071
	43	78	19.5	178670	9	AC104073
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	45	78	19.5	205130	2	AC105425

ALIGNMENTS

RESULT 1
BD272343 4186 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Methods of diagnosing or treating neurological diseases and cell degeneration.
ACCESSION BD272343.1 GI:33082111
VERSION UP 2002530076-A/3.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 4186)
Nitsch,R. and Greeve,I.
METHODS OF DIAGNOSING OR TREATING NEUROLOGICAL DISEASES AND CELL DEGENERATION
PATENT: JP 2002530076-A/3 17-SEP-2002;
JOURNAL
ROGER NITSCH, ISABELL GREVE
COMMENT
OS Homo sapiens (human)
PN UP 2002530076-A/3
PD 17-SEP-2002
PR 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREVE
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
PC A61P1/00,A61P15/00,A61P21/00,A61P25/00,A61P25/14,A61P25/16,
PC A61P25/28,
PC A61P43/00,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10,C12Q1/PC
68,
PC G01N33/53,G01N33/53,C12N15/00,C12N5/00,A61K37/02 CC Methods
of diagnosing or treating neurological diseases and CC
cell
CC degeneration
FH Key
FT source
Location/Qualifiers
1. 4186
/organism="Homo sapiens (human)"
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FEATURES

source

ORIGIN /db_xref="taxon:9606"

Query Match 100.0%; Score 400; DB 6; Length 4186;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCAACCCGAGCGCTTACCGCGCGCGCCGACCATGAGAGCCGCGTGTGCTG 60
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QY 61 CCGTGTGCGCGCTTCTTCTGCTGTGGTGGCGCTGAAGGGGCTGAGTTGCTGCTCA 120
DB 61 CCGTGTGCGCGCTTCTTCTGCTGTGGTGGCGCTGAAGGGGCTGAGTTGCTGCTCA 120
QY 121 TCCACGAGCGCGTGGGTGTGCTCTTCTCCGCGCGCTCTGCTTATCTTGATTA 180
DB 121 TCCACGAGCGCGTGGGTGTGCTCTTCTCCGCGCGCTCTGCTTATCTTGATTA 180
QY 181 TCTACTACTACGTGCGCGCTGGGTGTGTTCAAGCTCAGACAGCTCCGCGCTGACG 240
DB 181 TCTACTACTACGTGCGCGCTGGGTGTGTTCAAGCTCAGACAGCTCCGCGCTGACG 240
QY 241 AGCAGCGCGTGGCGGACATCCAGAGAGGTTGGGAAATGAAAGAGCAGGTTAGCA 300
DB 241 AGCAGCGCGTGGCGGACATCCAGAGAGGTTGGGAAATGAAAGAGCAGGTTAGCA 300
QY 301 CCTTCATGTGACGCGCGCGCTGGCGCTGCTCACTGTCTCACTACGTGTGGGAAGTACA 360
DB 301 CCTTCATGTGACGCGCGCGCTGGCGCTGCTCACTGTCTCACTACGTGTGGGAAGTACA 360
QY 361 AGAAGACACAAAACATCATGATCAACTGATGACAT 400
DB 361 AGAAGACACAAAACATCATGATCAACTGATGACAT 400

RESULT 2
AX026418 4186 bp DNA linear PAT 16-SEP-2000
LOCUS AX026418
DEFINITION Sequence 4 from Patent EP1002862.
ACCESSION AX026418
VERSION AX026418.1 GI:10187648
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Methods of diagnosing or treating neurological diseases
PATENT: EP 1002862-A 4 24-MAY-2000;
NITSCH ROGER M. PROF. DR. MED.
LOCATION/Qualifiers

FEATURES
source 1..4186
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 400; DB 6; Length 4186;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCAACCCGAGCGCTTACCGCGCGCGCCGACCATGAGAGCCGCGTGTGCTG 60
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QY 61 CCGTGTGCGCGCTTCTTCTGCTGTGGTGGCGCTGAAGGGGCTGAGTTGCTGCTCA 120
DB 61 CCGTGTGCGCGCTTCTTCTGCTGTGGTGGCGCTGAAGGGGCTGAGTTGCTGCTCA 120
QY 121 TCCACGAGCGCGTGGGTGTGCTCTTCTCCGCGCTCTGCTTATCTTGATTA 180
DB 121 TCCACGAGCGCGTGGGTGTGCTCTTCTCCGCGCTCTGCTTATCTTGATTA 180

DB 121 TCCACGAGCGCGTGGGTGTGCTCTTCTCCGCGCTCTGCTTATCTTGATTA 180
QY 181 TCTACTACTACGTGCGCGCTGGGTGTGTTCAAGCTCAGACAGCTCCGCGCTGACG 240
DB 181 TCTACTACTACGTGCGCGCTGGGTGTGTTCAAGCTCAGACAGCTCCGCGCTGACG 240
QY 241 AGCAGCGCGTGGCGGACATCCAGAGAGGTTGGGAAATGAAAGAGCAGGTTAGCA 300
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QY 301 CCTTCATGTGACGCGCGCGCTGGCGCTGCTCACTGTCTCACTACGTGTGGGAAGTACA 360
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QY 361 AGAAGACACAAAACATCATGATCAACTGATGACAT 400
DB 361 AGAAGACACAAAACATCATGATCAACTGATGACAT 400

RESULT 3
BD272342 4187 bp DNA linear PAT 17-JUL-2003
LOCUS BD272342
DEFINITION Methode of diagnosing or treating neurological diseases and cell
degeneration.
ACCESSION BD272342
VERSION BD272342.1 GI:33082110
KEYWORDS JP 2002530076-A/2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 4187)
Nitsch, R. and Greve, I.
Methode of diagnosing or treating neurological diseases and cell
degeneration
PATENT: JP 2002530076-A 2 17-SEP-2002;
ROGER NITSCH, ISABELL GREVE
OS Homo sapiens (human)
PN JP 2002530076-A/2

COMMENT
PD 17-SEP-2002 JP 2000582553
PF 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREVE
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
PC A61P1/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16,
PC A61P25/28,
PC A61P43/00, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, C1201/ PC

68, G01N33/53, G01N33/53, C12N15/00, C12N5/00, A61K37/02 CC Methods
of diagnosing or treating neurological diseases and CC
cell
degeneration
CC Key
FT source 1..4187
/organism="Homo sapiens (human)".

FEATURES
source 1..4187
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 400; DB 6; Length 4187;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCAACCCGAGCGCTTACCGCGCGCGCCGACCATGAGAGCCGCGTGTGCTG 60
DB 1 GGGCGCAACCCGAGCGCTTACCGCGCGCGCCGACCATGAGAGCCGCGTGTGCTG 60
QY 61 CCGTGTGCGCGCTTCTTCTGCTGTGGTGGCGCTGAAGGGGCTGAGTTGCTGCTCA 120
DB 61 CCGTGTGCGCGCTTCTTCTGCTGTGGTGGCGCTGAAGGGGCTGAGTTGCTGCTCA 120

Db 61 CCTTATGTCACGCGGGCCCTGCTGCTACTCTCTCACTGTCAGTGTGGGAAGTACA 360
QY 121 TCCACGACGCGCTGGGTGTGTGCTCTTCTCTCTGCGCTCTGCTTATCTTGATA 180
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QY 181 TCTACTACTAGTCGTCGCGCTGGGTGTGTGCTCTTCAAGCTCAAGCGCTTCCGCTGACG 240
Db 181 TCTACTACTAGTCGTCGCGCTGGGTGTGTGCTCTTCAAGCTCAAGCGCTTCCGCTGACG 240
QY 241 AGCAGCGCGTCGCGGACATCAGAGCAGGTCGCGGAATGGAAGACAGGATGACAGA 300
Db 241 AGCAGCGCGTCGCGGACATCAGAGCAGGTCGCGGAATGGAAGACAGGATGACAGA 300
QY 301 CCTTATGTCACGCGGGCCCTGCTGCTGCTCACTGTCAGTGTGGGAAGTACA 360
Db 361 AGAAGACACACAAAACATCATGATCACTGATGACAT 400
361 AGAAGACACACAAAACATCATGATCACTGATGACAT 400
RESULT 4
AX026417 4187 bp DNA linear PAT 16-SEP-2000
LOCUS AX026417
DEFINITION Sequence 3 from Patent EPI02862.
ACCESSION AX026417
VERSION AX026417.1 GI:10187647
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Methods of diagnosing or treating neurological diseases
TITLE Patent: EP 1002862-A 3 24-MAY-2000;
JOURNAL NITSCH ROGER M PROF DR (DE)
FEATURES
source 1. 4187
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 400; DB 6; Length 4187;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCGGAACCCGACGCTTACCGCGCGCGCGCACATGAGACCCGCGGTGCTGG 60
Db 1 GGGCGGAACCCGACGCTTACCGCGCGCGCGCACATGAGACCCGCGGTGCTGG 60
QY 61 CCGGTGCGCGCTCTTCTCTGCTGTGGTGGCTCTTCCCTGCGCTTCCCTTATCTTGATA 120
Db 61 CCGGTGCGCGCTCTTCTCTGCTGTGGTGGCTCTTCCCTGCGCTTCCCTTATCTTGATA 120
QY 121 TCCACGACGCGCTGGGTGTGTGCTCTTCTCTCTGCGCTCTGCTTATCTTGATA 180
Db 121 TCCACGACGCGCTGGGTGTGTGCTCTTCTCTCTGCGCTCTGCTTATCTTGATA 180
QY 181 TCTACTACTAGTCGTCGCGCTGGGTGTGTGCTCTTCAAGCTCAAGCGCTTCCGCTGACG 240
Db 181 TCTACTACTAGTCGTCGCGCTGGGTGTGTGCTCTTCAAGCTCAAGCGCTTCCGCTGACG 240
QY 241 AGCAGCGCGTCGCGGACATCAGAGCAGGTCGCGGAATGGAAGACAGGATGACAGA 300
Db 241 AGCAGCGCGTCGCGGACATCAGAGCAGGTCGCGGAATGGAAGACAGGATGACAGA 300
QY 301 CCTTATGTCACGCGGGCCCTGCTGCTGCTCACTGTCAGTGTGGGAAGTACA 360
301 CCTTATGTCACGCGGGCCCTGCTGCTGCTCACTGTCAGTGTGGGAAGTACA 360

Db 301 CCTTATGTCACGCGGGCCCTGCTGCTGCTCACTGTCAGTGTGGGAAGTACA 360
QY 361 AGAAGACACACAAAACATCATGATCACTGATGACAT 400
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RESULT 5
AX334630 4187 bp DNA linear PAT 09-JAN-2002
LOCUS AX334630
DEFINITION Sequence 5139 from Patent WO0194629.
ACCESSION AX334630
VERSION AX334630.1 GI:18125349
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 5139 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source 1. 4187
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCGGAACCCGACGCTTACCGCGCGCGCGCACATGAGACCCGCGGTGCTGG 60
Db 1 GGGCGGAACCCGACGCTTACCGCGCGCGCGCACATGAGACCCGCGGTGCTGG 60
QY 61 CCGGTGCGCGCTCTTCTCTGCTGTGGTGGCTCTTCCCTGCGCTTCCCTTATCTTGATA 120
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QY 121 TCCACGACGCGCTGGGTGTGTGCTCTTCTCTCTGCGCTCTGCTTATCTTGATA 180
Db 121 TCCACGACGCGCTGGGTGTGTGCTCTTCTCTCTGCGCTCTGCTTATCTTGATA 180
QY 181 TCTACTACTAGTCGTCGCGCTGGGTGTGTGCTCTTCAAGCTCAAGCGCTTCCGCTGACG 240
Db 181 TCTACTACTAGTCGTCGCGCTGGGTGTGTGCTCTTCAAGCTCAAGCGCTTCCGCTGACG 240
QY 241 AGCAGCGCGTCGCGGACATCAGAGCAGGTCGCGGAATGGAAGACAGGATGACAGA 300
Db 241 AGCAGCGCGTCGCGGACATCAGAGCAGGTCGCGGAATGGAAGACAGGATGACAGA 300
QY 301 CCTTATGTCACGCGGGCCCTGCTGCTGCTCACTGTCAGTGTGGGAAGTACA 360
Db 301 CCTTATGTCACGCGGGCCCTGCTGCTGCTCACTGTCAGTGTGGGAAGTACA 360
QY 361 AGAAGACACACAAAACATCATGATCACTGATGACAT 400
361 AGAAGACACACAAAACATCATGATCACTGATGACAT 400
RESULT 6
AX408962 4187 bp DNA linear PAT 14-JUN-2002
LOCUS AX408962
DEFINITION Sequence 1609 from Patent WO0229103.
ACCESSION AX408962
VERSION AX408962.1 GI:21441667
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM	Homio sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1
TITLE	Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
JOURNAL	Gene expression profiles in liver cancer
GENE	Patent: WO 0229103-A 1609 11-APR-2002;
LOGIC	GENE LOGIC INC (US)
LOCATION/Qualifiers	1. .4187
ORGANISM	"/organism="Homo sapiens"
mol_type	"/mol_type="unassigned DNA"
db_xref	"/db_xref="taxon:9606"
note	"/note="EMBL/GenBank Accession No. D13643"
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Query Match	100.0%; Score 400; DB 6; Length 4187;
Best Local Similarity	100.0%; Pred. No. 1.8e-67;
Matches	400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GGGCGGAACCCGACCGCTTACCGGGGGGGCCGACCATATGAGCCCGCTGTGCTGG 60
DB	1 GGGCGGAACCCGACCGCTTACCGGGGGGGCCGACCATATGAGCCCGCTGTGCTGG 60
QY	61 CCGTGTGGCGCGCTGCTTCTTCCGTGTGGGTGGCGGCTGAAGGGGGTGAGTTGCGTCA 120
DB	61 CCGTGTGGCGCGCTGCTTCTTCCGTGTGGGTGGCGGCTGAAGGGGGTGAGTTGCGTCA 120
QY	121 TCCACGACGCGTGGGTGTTGCTGTGTCCTTCTCTCCTGCGCTGTGCTTATCTTCGATA 180
DB	121 TCCACGACGCGTGGGTGTTGCTGTGTCCTTCTCTCCTGCGCTGTGCTTATCTTCGATA 180
QY	181 TCTACTTACTACGTGGGGCGCTGGGTGTGTTCAAGCTAGACAGCGCTCCGGCGCTGACAG 240
DB	181 TCTACTTACTACGTGGGGCGCTGGGTGTGTTCAAGCTAGACAGCGCTCCGGCGCTGACAG 240
QY	241 AGCAGCGCGTGGGGGACATCCAGAGCAGGTGGCGGAATGGAAGAGAGAGGATAGACA 300
DB	241 AGCAGCGCGTGGGGGACATCCAGAGCAGGTGGCGGAATGGAAGAGAGGATAGACA 300
QY	301 CCTTCATGTGACAGGGGGCGCCCTGGCTGACTGTCTCACTACGTGTGGGGAAGTACA 360
DB	301 CCTTCATGTGACAGGGGGCGCCCTGGCTGACTGTCTCACTACGTGTGGGGAAGTACA 360
QY	361 AGAAGACACACAAAACATCATGATCAACCTGATGGAAT 400
DB	361 AGAAGACACACAAAACATCATGATCAACCTGATGGAAT 400
RESULT 7	
AX828407	4187 bp DNA linear PAT 12-DEC-2003
LOCUS	AX828407
DEFINITION	Sequence 53 from Patent WO03074073.
ACCESSION	AX828407
VERSION	AX828407.1 GI:39838407
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
mol_type	Homio sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
Al-Mahmood, S., Collin, S. and Schneider, C.	
Genes involved in regulating angiogenesis, pharmaceutical	
preparations containing same and applications thereof	
Patent: WO 03074073-A 53 12-SEP-2003;	
Gene Signal (FR)	
Location/Qualifiers	1. .4187
ORGANISM	"/organism="Homo sapiens"
mol_type	"/mol_type="unassigned DNA"
db_xref	"/db_xref="taxon:9606"
ORIGIN	

Query Match	100.0%	Score 400	DB 6	Length 4187
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Qy	1	GGCGGGAACCCGGAGCGCTTACCGCGCGCGCCGACCATGAGCCCGCGGTGCTGG	60	
Db	1	GGCGGGAACCCGGAGCGCTTACCGCGCGCGCCGACCATGAGCCCGCGGTGCTGG	60	
Qy	61	CCGTGTCCGCGGCTCTTCTTCTGTGGGTGGCGCTGAAGGGGCTGGAGTTGCTCA	120	
Db	61	CCGTGTCCGCGGCTCTTCTTCTGTGGGTGGCGCTGAAGGGGCTGGAGTTGCTCA	120	
Qy	121	TTCAACCAAGCGCTGGGTGTGTGTGCTCTTCCGCGCGCGCTGTGCTTATCTGGATA	180	
Db	121	TTCAACCAAGCGCTGGGTGTGTGTGCTCTTCCGCGCGCGCTGTGCTTATCTGGATA	180	
Qy	181	TTCTACTACTAGTCGCGCGCTGGGTGGTGTTCATGACTCAGACAGCGCTCCGCGCTGACG	240	
Db	181	TTCTACTACTAGTCGCGCGCTGGGTGGTGTTCATGACTCAGACAGCGCTCCGCGCTGACG	240	
Qy	241	AGCAGCGCGTGGCGGACATTCAGAGCAGGTGGCGGATGGAAGACAGCGGTATGACAGA	300	
Db	241	AGCAGCGCGTGGCGGACATTCAGAGCAGGTGGCGGATGGAAGACAGCGGTATGACAGA	300	
Qy	301	CCCTTCATGTCACAGGGGCGCGCTGGCGTGCCTACTGCTCATACGTTGTGGGGAATGACA	360	
Db	301	CCCTTCATGTCACAGGGGCGCGCTGGCGTGCCTACTGCTCATACGTTGTGGGGAATGACA	360	
Qy	361	AGAAGACACACAAAACATCATGATCAACCTGATGAGCAT 400		
Db	361	AGAAGACACACAAAACATCATGATCAACCTGATGAGCAT 400		
RESULT 8				
LOCUS	HUMRSC390	4187 bp	mRNA	linear PRI 06-OCT-2001
ACCESSION	D13643			
VERSION	D13643.2	GI:6630631		
KEYWORDS	K1AA0018 protein.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1		
AUTHORS	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
TITLE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
JOURNAL	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
MEDLINE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
PUBMED	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
REFERENCE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
AUTHORS	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
TITLE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
JOURNAL	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
MEDLINE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
PUBMED	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
REFERENCE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
AUTHORS	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
TITLE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
JOURNAL	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
MEDLINE	1	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by		

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Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGGAACCCGCGAGCGCTTACCGCGGCGCGCGACCATGAGACCCGCGTGCCTGG 60
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RESULT 9
BD272341 4248 bp DNA linear PAT 17-JUL-2003
LOCUS BD272341
DEFINITION Methods of diagnosing or treating neurological diseases and cell
degeneration.
ACCESSION BD272341
VERSION BD272341.1 GI:33082109
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KEYWORDS
SOURCE JP 2002530076-A/1.
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 4248)
Nucleic acid sequence of human chromosome 1.
METHODS Methods of diagnosing or treating neurological diseases and cell
degeneration
JOURNAL Patient: JP 2002530076-A 1 17-SEP-2002;
COMMENT ROGER NITSCH, ISABELL GREVE
OS Homo sapiens (human)
PN JP 2002530076-A/1
PD 17-SEP-2002 JP 2000582553
PF 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREVE
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
A61P11/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16,
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of diagnosing or treating neurological diseases and CC
cell degeneration
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Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 302 AGCAGCGGCGGCGGACATCCAGAGAGAGTGGGGAATGGAAGAGAGGAGTGAAGA 361
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DEFINITION Sequence 329 from Patent EP1394274.
ACCESSION CO776643
VERSION CO776643.1 GI:45380033
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
JOURNAL Patent: EP 1394274-A 329 03-MAR-2004;
Genex Research, Inc. (JP)
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Query Match 100.0%; Score 400; DB 6; Length 4248;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCGGCAACCCGAGCGCTTACCGCGCGCGCGCAACATGAGCCCGCGTGCCTG 60
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DB 422 AGAAGACACACAAAACATCATGATCAACCTGATGACAT 461
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DEFINITION Sequence 526 from Patent EP1394274.
ACCESSION CO776840
VERSION CO776840.1 GI:45380230
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
JOURNAL Patent: EP 1394274-A 526 03-MAR-2004;
Genex Research, Inc. (JP)
FEATURES
Location/Qualifiers

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QY 1 GGCGGCAACCCGAGCGCTTACCGCGCGCGCGCAACATGAGCCCGCGTGCCTG 60
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QY 61 CGGTGCGCGCTGCTCTTCTGCTGTGGTGCCTGAGAGGGAGTTCGTCTCA 120
DB 122 CGGTGCGCGCTGCTCTTCTGCTGTGGTGCCTGAGAGGGAGTTCGTCTCA 181
QY 121 TCACACAGCGCTGGGTGTGTGTGCTCTTCTCCCGCGCTGCTGCTTATCTTGATA 180
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DB 422 AGAAGACACACAAAACATCATGATCAACCTGATGACAT 461
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DEFINITION Sequence 2 from Patent EP1002862.
ACCESSION AX026416
VERSION AX026416.1 GI:10187646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NITSCH ROGER M PROF DR (DE)
TITLE Methods of diagnosing or treating neurological diseases
JOURNAL Patent: EP 1002862-A 2 24-MAY-2000;
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QY 1 GGCGGCAACCCGAGCGCTTACCGCGCGCGCGCAACATGAGCCCGCGTGCCTG 60
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QY 61 CGGTGCGCGCTGCTCTTCTGCTGTGGTGCCTGAGAGGGAGTTCGTCTCA 120
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QY	181	TCCTACTACTAGTGGCGCCCTGGTGGTGTGTTCTCAAGCTCAGCAGCGCTCCGCGCTGCACG	240
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QY	241	AGCAGCGCGTCCGGGACATCCAGGAAGAGTGGCGGAAATGGAAAGAGCAGGGTATGACAGA	300
Db	302	AGCAGCGCGTCCGGGACATCCAGGAAGAGTGGCGGAAATGGAAAGAGCAGGGTATGACAGA	361
QY	301	CCCTTCATGTGACCGGGGCGCCCTGGCTGACTCATCTGTCTCACTACGTGTGGGAAGTACA	360
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ACCESSION	AX828386			linear
VERSION	AX828386.1			PAT 12-DEC-2003
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Al-Mahmoud, S., Colin, S. and Schneider, C.	Genes involved in regulating angiogenesis, pharmaceutical preparations containing same and applications thereof	Patent: WO 03074073-A 32 12-SEP-2003;

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ACCESSION	AF261758
VERSION	AF261758.1
GI	10442024

ORGANISM	SOURCE	TEST METHODS
Homo sapiens	Homo sapiens (human)	

REFERENCE
1 (bases 1 to 4248)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

TITLE	Author
Gomez-Isla, T., Behl, C., Levkau, B. and Nitsch, R.M. The human DIMINUTO/DWARF1 homolog seladin-1 confers resistance to	10

stress
J. Neurosci. 20 (19), 7345-7352 (2000)
20482303

FORMED	1100/892
REFERENCE	2 (bases 1 to 4248)
AUTHORS	Greeve, I.

JOURNAL
Submitted (28-APR-2000) Center for Molecular Neurobiology
Martinistrasse 52, Hamburg 20246, Germany

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ORIGIN

Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION
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MGC:15380 IMAGE:4130396), complete cds.
BC011669
* ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 4254)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, J., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, T.E., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrams, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Boutfair, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalske, U., Smalls, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
JOURNAL
PUBMED
2 (bases 1 to 4254)
Straussberg, R.
REFERENCE
AUTHORS
TITLE
JOURNAL
DIRECT SUBMISSION
Submitted (30-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:15079698.
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gallagherburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akheri, N., Boufard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Boufard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
Maduro, O.L., Mastello, C., Maskeri, B., Mastrian, S.D., McElroy, J.C.,

McDowell, J., Pearson, R., Stantipod, S., Thomas, P.J., Touchman, J.W.,
Taugen, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAL Plates: 26 Row: 1 Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
Location/Qualifiers

FEATURES

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CDS

ORIGIN
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